

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2005, 11:22:43 ; Search time 17.8241 Seconds  
(without alignments)  
770.608 Million cell updates/sec

Title: US-10-629-516-2\_COPY\_10\_193

Perfect score: 943  
Sequence: 1 CNAPRWVSLMVLVAIGTAVT.....HVHISKSKVGLIQLPHKKI 184

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTCUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	943	100.0	243	1	US-07-915-720D-16
2	943	100.0	243	3	US-09-025-543-16
3	943	100.0	262	4	US-09-949-016-9146
4	943	100.0	300	1	US-08-218-026-2
5	943	100.0	300	2	US-08-653-632-2
6	943	100.0	368	1	US-07-915-720D-15
7	943	100.0	368	3	US-09-025-543-15
8	943	100.0	483	4	US-09-578-063-38
9	943	100.0	487	1	US-08-030-644-2
10	943	100.0	487	1	US-08-013-801-2
11	943	100.0	487	1	US-08-072-063-2
12	943	100.0	487	1	US-08-212-132-2
13	943	100.0	487	1	US-08-414-924-2
14	943	100.0	487	1	US-08-311-611A-69
15	943	100.0	487	1	US-08-311-611A-146
16	943	100.0	487	1	US-08-173-968-2
17	943	100.0	487	1	US-08-232-527-2
18	943	100.0	487	1	US-08-372-783-69
19	943	100.0	487	1	US-08-372-783-146
20	943	100.0	487	1	US-08-372-105-69
21	943	100.0	487	1	US-08-372-105-146
22	943	100.0	487	1	US-08-415-158-2
23	943	100.0	487	1	US-08-064-693-2
24	943	100.0	487	1	US-08-291-112-2
25	943	100.0	487	1	US-08-306-473A-69
26	943	100.0	487	1	US-08-306-473A-146
27	943	100.0	487	1	US-08-430-417-2

28	943	100.0	487	1	US-08-557-287-2	Sequence 2, Appli
29	943	100.0	487	1	US-08-470-366-2	Sequence 2, Appli
30	943	100.0	487	1	US-08-261-660A-12	Sequence 12, Appl
31	943	100.0	487	1	US-08-209-762-69	Sequence 69, Appl
32	943	100.0	487	1	US-08-644-290-2	Sequence 2, Appli
33	943	100.0	487	1	US-08-378-228-2	Sequence 2, Appli
34	943	100.0	487	1	US-08-927-438-2	Sequence 2, Appli
35	943	100.0	487	1	US-08-473-344-69	Sequence 69, Appl
36	943	100.0	487	1	US-08-274-303-2	Sequence 2, Appli
37	943	100.0	487	1	US-07-915-720D-13	Sequence 13, Appl
38	943	100.0	487	1	US-08-218-026-4	Sequence 4, Appli
39	943	100.0	487	1	US-08-435-855-2	Sequence 2, Appli
40	943	100.0	487	2	US-08-466-822-2	Sequence 2, Appli
41	943	100.0	487	2	US-08-653-632-4	Sequence 4, Appli
42	943	100.0	487	2	US-08-466-624-2	Sequence 2, Appli
43	943	100.0	487	2	US-08-621-803-265	Sequence 265, App
44	943	100.0	487	2	US-08-466-826-2	Sequence 2, Appli
45	943	100.0	487	2	US-08-704-504-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-07-915-720D-16  
; Sequence 16, Application US/07915720D  
; Patent No. 5,770,694  
; GENERAL INFORMATION:  
; APPLICANT: Scott, Randal W.  
; APPLICANT: Maria, Marian N.  
; TITLE OF INVENTION: GENETICALLY ENGINEERED BPI VARIANT  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 2200 Sand Hill Road, Suite 100  
; CITY: Menlo Park  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/915,720D  
; FILING DATE: 22-JUL-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Francis, Carol L.  
; REGISTRATION NUMBER: 36,513  
; REFERENCE/POCKET NUMBER: 06514/030001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/322-5070  
; TELEFAX: 415/854-0875  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 243 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-915-720D-16

Query Match 100.0%; Score 943; DB 1; Length 243;  
Best Local Similarity 100.0%; Pred. No. 4.7e-70;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CNAPRWVSLMVLVAIGTAVTA	VNPGVVVRISQKGLDYASQOGTAALQKELKRIKIPDYS 60
DB	10	CNAPRWVSLMVLVAIGTAVTA	VNPGVVVRISQKGLDYASQOGTAALQKELKRIKIPDYS 69

QY 61 DPFKIKHLGKGHYSFYSMDIREFOLPSSQISMPVNVGLKFSISNANIKISGKKAQKRFL 120  
Db 70 DPFKIKHLGKGHYSFYSMDIREFOLPSSQISMPVNVGLKFSISNANIKISGKKAQKRFL 129  
QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHHSKSKVGLIQLF 180  
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHHSKSKVGLIQLF 189  
QY 181 HKKI 184  
Db 190 HKKI 193

RESULT 2  
US-09-025-543-16  
; Sequence 16, Application US/09025543  
; Patent No. 6093801  
; GENERAL INFORMATION:  
; APPLICANT: Scott, Randal W.  
; TITLE OF INVENTION: GENETICALLY ENGINEERED BPI VARIANT  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bozicevic & Reed, LLP  
; STREET: 285 Hamilton, Suite 200  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,543  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Francis, Carol L.  
; REGISTRATION NUMBER: 36,513  
; REFERENCE/DOCKET NUMBER: 06514/030005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/327-3400  
; TELEFAX: 650/327-3231  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 243 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-025-543-16

Query Match 100.0%; Score 943; DB 3; Length 243;  
Best Local Similarity 100.0%; Pred. No. 4.7e-70;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNAPRWVSLMVLVAIGTAVTAANNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 60  
Db 10 CNAPRWVSLMVLVAIGTAVTAANNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 69  
QY 61 DPFKIKHLGKGHYSFYSMDIREFOLPSSQISMPVNVGLKFSISNANIKISGKKAQKRFL 120  
Db 70 DPFKIKHLGKGHYSFYSMDIREFOLPSSQISMPVNVGLKFSISNANIKISGKKAQKRFL 129  
QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHHSKSKVGLIQLF 180  
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHHSKSKVGLIQLF 189  
QY 181 HKKI 184  
Db 190 HKKI 193

Db 190 HKKI 193

RESULT 3  
US-09-949-016-9146  
; Sequence 9146, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9146  
; LENGTH: 262  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-9146

Query Match 100.0%; Score 943; DB 4; Length 262;  
Best Local Similarity 100.0%; Pred. No. 5.1e-70;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNAPRWVSLMVLVAIGTAVTAANNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 60  
Db 33 CNAPRWVSLMVLVAIGTAVTAANNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 92  
QY 61 DPFKIKHLGKGHYSFYSMDIREFOLPSSQISMPVNVGLKFSISNANIKISGKKAQKRFL 120  
Db 93 DPFKIKHLGKGHYSFYSMDIREFOLPSSQISMPVNVGLKFSISNANIKISGKKAQKRFL 152  
QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHHSKSKVGLIQLF 180  
Db 153 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHHSKSKVGLIQLF 212  
QY 181 HKKI 184  
Db 213 HKKI 216

RESULT 4  
US-08-218-026-2  
; Sequence 2, Application US/08218026  
; Patent No. 5786324  
; GENERAL INFORMATION:  
; APPLICANT: Gray, Beulah  
; APPLICANT: Hasegan, Judith R.  
; APPLICANT: Mayo, Kevin  
; TITLE OF INVENTION: Synthetic Peptides with Bactericidal  
; Activity and Endotoxin Neutralizing Activity for Gram  
; Negative Bacteria and Methods for Their Use  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 3100 No. 5786324west Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/218,026
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kowalchuk, Katherine M.
; REGISTRATION NUMBER: 36,848
; REFERENCE/DOCKET NUMBER: 600.286US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-5081
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 300 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-218-026-2

Query Match 100.0%; Score 943; DB 1; Length 300;
Best Local Similarity 100.0%; Pred. No. 5.9e-70;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQGTAAALQKELKRIKIPDYS 60
DB 10 CNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQGTAAALQKELKRIKIPDYS 69
QY 61 DSFKIKHLKGHYSPYMDIREFQLPSSQISMVNVNGLKFSISNANIKISGKWKAKQKRF 120
DB 70 DSFKIKHLKGHYSPYMDIREFQLPSSQISMVNVNGLKFSISNANIKISGKWKAKQKRF 129
QY 121 KMSGNFDLSIEGMSIADLKLSNPTSGKPTTICSSSHINSVHVHISKSVGWLILQF 180
DB 130 KMSGNFDLSIEGMSIADLKLSNPTSGKPTTICSSSHINSVHVHISKSVGWLILQF 189
QY 181 HKKI 184
DB 190 HKKI 193

RESULT 5
US-08-653-632-2
; Sequence 2, Application US/08653632
; Patent No. 5830860
; GENERAL INFORMATION:
; APPLICANT: GRAY, Beulah
; APPLICANT: HASEMAN, Judith R.
; APPLICANT: MAYO, Kevin
; TITLE OF INVENTION: PEPTIDES WITH BACTERICIDAL AND ENDOTOXIN NEUTRALIZING
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 5830860west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/653,632
; FILING DATE: 24-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/218026
; FILING DATE: 24-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kettelberger, Denise M
; REGISTRATION NUMBER: 33,924
; REFERENCE/DOCKET NUMBER: 600.286US11

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5268
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 300 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-653-632-2

Query Match 100.0%; Score 943; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 5.9e-70;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQGTAAALQKELKRIKIPDYS 60
DB 10 CNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQGTAAALQKELKRIKIPDYS 69
QY 61 DSFKIKHLKGHYSPYMDIREFQLPSSQISMVNVNGLKFSISNANIKISGKWKAKQKRF 120
DB 70 DSFKIKHLKGHYSPYMDIREFQLPSSQISMVNVNGLKFSISNANIKISGKWKAKQKRF 129
QY 121 KMSGNFDLSIEGMSIADLKLSNPTSGKPTTICSSSHINSVHVHISKSVGWLILQF 180
DB 130 KMSGNFDLSIEGMSIADLKLSNPTSGKPTTICSSSHINSVHVHISKSVGWLILQF 189
QY 181 HKKI 184
DB 190 HKKI 193

RESULT 6
US-07-915-720D-15
; Sequence 15, Application US/07915720D
; Patent No. 5770694
; GENERAL INFORMATION:
; APPLICANT: Scott, Randal W.
; APPLICANT: Marra, Marian N.
; TITLE OF INVENTION: GENETICALLY ENGINEERED BPI VARIANT
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/915,720D
; FILING DATE: 22-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Francis, Carol L.
; REGISTRATION NUMBER: 36,513
; REFERENCE/DOCKET NUMBER: 06514/030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/322-5070
; TELEFAX: 415/854-0875
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:

```

```
; LENGTH: 368 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-915-720D-15

Query Match      100.0%; Score 943; DB 1; Length 368;
Best Local Similarity 100.0%; Pred. No. 7.3e-70;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQOGTAALQKELKRIKIPDYS 60
   |||||
Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQOGTAALQKELKRIKIPDYS 69

Qy 61 DPFKIKHLGKGHYSFYSMDIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKRFL 120
   |||||
Db 70 DPFKIKHLGKGHYSFYSMDIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKRFL 129

Qy 121 KMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKVGWLIQLF 180
   |||||
Db 130 KMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKVGWLIQLF 189

Qy 181 HKKI 184
   ||||
Db 190 HKKI 193

RESULT 7
US-09-025-543-15
; Sequence 15, Application US/09025543
; Patent No. 6093801
; GENERAL INFORMATION:
; APPLICANT: Scott, Randal W.
; APPLICANT: Marra, Marian N.
; TITLE OF INVENTION: GENETICALLY ENGINEERED BPI VARIANT
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/025.543
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Francis, Carol L.
; REGISTRATION NUMBER: 36,513
; REFERENCE/DOCKET NUMBER: 06514/030005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/327-3400
; TELEFAX: 650/327-3231
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 368 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-543-15

Query Match      100.0%; Score 943; DB 3; Length 368;
Best Local Similarity 100.0%; Pred. No. 7.3e-70;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQOGTAALQKELKRIKIPDYS 60
   |||||
Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQOGTAALQKELKRIKIPDYS 69

Qy 61 DPFKIKHLGKGHYSFYSMDIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKRFL 120
   |||||
Db 70 DPFKIKHLGKGHYSFYSMDIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKRFL 129

Qy 121 KMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKVGWLIQLF 180
   |||||
Db 130 KMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKVGWLIQLF 189

Qy 181 HKKI 184
   ||||
Db 190 HKKI 193

Query Match      100.0%; Score 943; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 9.8e-70;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQOGTAALQKELKRIKIPDYS 60
   |||||
Db 6 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQOGTAALQKELKRIKIPDYS 65

Qy 61 DPFKIKHLGKGHYSFYSMDIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKRFL 120
   |||||
Db 66 DPFKIKHLGKGHYSFYSMDIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKRFL 125

Qy 121 KMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKVGWLIQLF 180
   |||||
Db 126 KMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKVGWLIQLF 185

Qy 181 HKKI 184
   ||||
Db 186 HKKI 189

RESULT 8
US-09-578-063-38
; Sequence 38, Application US/09578063
; Patent No. 6764677
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A
; APPLICANT: Barnes, Thomas M
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
; FILE REFERENCE: 210147.0023/6U1
; CURRENT APPLICATION NUMBER: US/09/578.063
; CURRENT FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333.159
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-578-063-38

Query Match      100.0%; Score 943; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 9.8e-70;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQOGTAALQKELKRIKIPDYS 60
   |||||
Db 6 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQOGTAALQKELKRIKIPDYS 65

Qy 61 DPFKIKHLGKGHYSFYSMDIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKRFL 120
   |||||
Db 66 DPFKIKHLGKGHYSFYSMDIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKRFL 125

Qy 121 KMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKVGWLIQLF 180
   |||||
Db 126 KMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKVGWLIQLF 185

Qy 181 HKKI 184
   ||||
Db 186 HKKI 189

RESULT 9
US-08-030-644-2
; Sequence 2, Application US/08030644
; Patent No. 5348942
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G. II
; APPLICANT: Gazzano-Santoro, Helene
; APPLICANT: Parent, James Brian
; TITLE OF INVENTION: Therapeutic uses of
; Bactericidal/Permeability-Increasing Protein Products
```



NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/030,644  
FILING DATE: 19930312  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharp, Jeffrey S.  
REGISTRATION NUMBER: 31,879  
REFERENCE/DOCKET NUMBER: 31229  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-030-644-2

Query Match 100.0%; Score 943; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 9.9e-70;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CNAPRWLSLMLVLAIGTAVTAANVPGVVVRISQKGLDYASQOGTAALQKELKRIKIPDYS 60  
DB 10 CNAPRWLSLMLVLAIGTAVTAANVPGVVVRISQKGLDYASQOGTAALQKELKRIKIPDYS 69  
  
QY 61 DSFKIKHLKGHYSPYMDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFL 120  
DB 70 DSFKIKHLKGHYSPYMDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFL 129  
  
QY 121 KMSGNFDLSIEGMSISADLKLSNPTSGKPTITCSCSSHNSVHVHISKSKVGLIQLF 180  
DB 130 KMSGNFDLSIEGMSISADLKLSNPTSGKPTITCSCSSHNSVHVHISKSKVGLIQLF 189  
  
QY 181 HKKI 184  
DB 190 HKKI 193

RESULT 10  
US-08-013-801-2  
Sequence 2, Application US/08013801  
Patent No. 5420019  
GENERAL INFORMATION:  
APPLICANT: Theofan, Georgia  
APPLICANT: Horwitz, Arnold  
APPLICANT: Burke, David  
APPLICANT: Baltayan, Manik  
APPLICANT: Grinna, Lynn S  
TITLE OF INVENTION: Stable Bactericidal/Permeability-  
TITLE OF INVENTION: Increasing Protein Products and Pharmaceutical  
TITLE OF INVENTION: Compositions Containing the Same  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza  
CITY: Chicago

STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/013,801  
FILING DATE: 02 FEB 1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Thomas C.  
REGISTRATION NUMBER: P-36,989  
REFERENCE/DOCKET NUMBER: 27129/30911  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/346-5750  
TELEFAX: 312/346-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-013-801-2

Query Match 100.0%; Score 943; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 9.9e-70;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CNAPRWLSLMLVLAIGTAVTAANVPGVVVRISQKGLDYASQOGTAALQKELKRIKIPDYS 60  
DB 10 CNAPRWLSLMLVLAIGTAVTAANVPGVVVRISQKGLDYASQOGTAALQKELKRIKIPDYS 69  
  
QY 61 DSFKIKHLKGHYSPYMDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFL 120  
DB 70 DSFKIKHLKGHYSPYMDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFL 129  
  
QY 121 KMSGNFDLSIEGMSISADLKLSNPTSGKPTITCSCSSHNSVHVHISKSKVGLIQLF 180  
DB 130 KMSGNFDLSIEGMSISADLKLSNPTSGKPTITCSCSSHNSVHVHISKSKVGLIQLF 189  
  
QY 181 HKKI 184  
DB 190 HKKI 193

RESULT 11  
US-08-072-063-2  
Sequence 2, Application US/08072063  
Patent No. 5439807  
GENERAL INFORMATION:  
APPLICANT: Theofan, Georgia  
APPLICANT: Grinna, Lynn S  
APPLICANT: Horwitz, Arnold  
TITLE OF INVENTION: BPI-Immunoglobulin Fusion Proteins  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/072,063

```
; FILING DATE: 19930519
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers Thomas C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: 30659
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-072-063-2

Query Match 100.0%; Score 943; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 9.9e-70;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 60
Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 69

Qy 61 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISMPNVGLKFSISNANIKISGKWKAKRFL 120
Db 70 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISMPNVGLKFSISNANIKISGKWKAKRFL 129

Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKVGWLIQLF 180
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKVGWLIQLF 189

Qy 181 HKKI 184
Db 190 HKKI 193

RESULT 12
US-08-212-132-2
; Sequence 2, Application US/08212132
; Patent No. 5447913
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G.
; APPLICANT: Ammons, William Steve
; TITLE OF INVENTION: Therapeutic Uses of Bactericidal/Permeability-
; TITLE OF INVENTION: Increasing Protein Dimer Products
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,132
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/31735
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-072-063-2

Query Match 100.0%; Score 943; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 9.9e-70;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 60
Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 69

Qy 61 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISMPNVGLKFSISNANIKISGKWKAKRFL 120
Db 70 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISMPNVGLKFSISNANIKISGKWKAKRFL 129

Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKVGWLIQLF 180
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKVGWLIQLF 189

Qy 181 HKKI 184
Db 190 HKKI 193

RESULT 13
US-08-414-924-2
; Sequence 2, Application US/08414924
; Patent No. 5494896
; GENERAL INFORMATION:
; APPLICANT: Hansbrough, John F.
; TITLE OF INVENTION: Method of Treating Conditions
; TITLE OF INVENTION: Associated With Burn Injuries
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,924
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/32297
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-414-924-2

Query Match 100.0%; Score 943; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 9.9e-70;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 60
Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 69

Qy 61 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISMPNVGLKFSISNANIKISGKWKAKRFL 120
Db 70 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISMPNVGLKFSISNANIKISGKWKAKRFL 129

Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKVGWLIQLF 180
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKVGWLIQLF 189

Qy 181 HKKI 184
Db 190 HKKI 193
```

	Matches	184;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	CNAPRWSLMVLVAIGTAVTA	AAVNP	GVVV	RSQKGLDYASQOGTAALQKELKRIKIPDYS	60				
Db	10	CNAPRWSLMVLVAIGTAVTA	AAVNP	GVVV	RSQKGLDYASQOGTAALQKELKRIKIPDYS	69				
Qy	61	DSPKIKHLGKGYGFYSNDIRE	FOLP	SSQIS	MPNVNGIKFSGISNANIKISKGKWAQKRF	120				
Db	70	DSPKIKHLGKGYGFYSNDIRE	FOLP	SSQIS	MPNVNGIKFSGISNANIKISKGKWAQKRF	129				
Qy	121	KMSGNFOLSIIEGMSITADL	KLGSNPT	SGKPI	TTSCSSSHSTNSVHVHISKSVGWLIOLF	180				
Db	130	KMSGNFOLSIIEGMSITADL	KLGSNPT	SGKPI	TTSCSSSHSTNSVHVHISKSVGWLIOLF	189				
Qy	181	HKKI	184							
Db	190	HKKI	193							

RESULT 14  
US-08-311-611A-69  
Sequence 69, Application US/08311611A  
Patent No. 5523288  
GENERAL INFORMATION:  
APPLICANT: Cohen, Jonathan  
APPLICANT: Kung, Ada H.C.  
APPLICANT: Lambert, Jr., Lewis H.  
TITLE OF INVENTION: Method for Treating Gram-Negative Bacterial  
TITLE OF INVENTION: Infection by Administration of  
TITLE OF INVENTION: Bactericidal/Permeability-Increasing  
TITLE OF INVENTION:  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/311,611A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/273,401  
FILING DATE: 11-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/125,651  
FILING DATE: 22-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharp, Jeffrey S.  
REGISTRATION NUMBER: 31,879  
REFERENCE/DOCKET NUMBER: 32251  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: "rBPI"  
US-08-311-611A-69

Query Match 100.0%; Score 943; DB 1; Length 487;

Query Match 100.0%; Score 943; DB 1; Length 487;

```
Query Match      100.0%; Score 943; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. NO. 9.9e-70;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0
```

0 Gaps

Qy	1	CNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOGTAALQKELKRIKIPDYS	60
Db	10	CNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOGTAALQKELKRIKIPDYS	69
Qy	61	DSPKIKHLGKGHSFYSDIREFOLPSSQISMVFNVLKFSISNANIKISGKWKAKRFL	120
Db	70	DSPKIKHLGKGHSFYSDIREFOLPSSQISMVFNVLKFSISNANIKISGKWKAKRFL	129
Qy	121	KMSGNFDLSIEGMSISADLKLGNPTSGKPTITCSCSSHINSVHVHISKSKVGWLIQLF	180
Db	130	KMSGNFDLSIEGMSISADLKLGNPTSGKPTITCSCSSHINSVHVHISKSKVGWLIQLF	189
Qy	181	HKXI 184	
Db	190	HKXI 193	

Search completed: October 21, 2005, 11:32:58  
Job time : 18.8241 secs

Fri Oct 21 12:25:52 2005

NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/030.644  
FILING DATE: 19930312  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharp, Jeffrey S.  
REGISTRATION NUMBER: 31,879  
REFERENCE/DOCKET NUMBER: 31229  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-030-644-2

Query Match 100.0%; Score 943; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 9.9e-70;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CNAFRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQGGTAALQKELKRIKIPDYS 60  
Db 10 CNAFRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQGGTAALQKELKRIKIPDYS 69  
  
Qy 61 DSFKIKHLGKHGHSFYSDMIREFQLPSSQISMPVNVGLKFSISNANIKISGKWKAKRFL 120  
Db 70 DSFKIKHLGKHGHSFYSDMIREFQLPSSQISMPVNVGLKFSISNANIKISGKWKAKRFL 129  
  
Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHLSKSKVGLIQLF 180  
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHLSKSKVGLIQLF 189  
  
Qy 181 HKKI 184  
Db 190 HKKI 193

RESULT 10  
US-08-013-801-2  
Sequence 2, Application US/08013801  
Patent No. 5420019  
GENERAL INFORMATION:  
APPLICANT: Theofan, Georgia  
APPLICANT: Horwitz, Arnold  
APPLICANT: Burke, David  
APPLICANT: Baltaian, Manik  
APPLICANT: Grinna, Lynn S  
TITLE OF INVENTION: Stable Bactericidal/Permeability-  
Increasing Protein Products and Pharmaceutical  
TITLE OF INVENTION: Compositions Containing the Same  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza  
CITY: Chicago

STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/013.801  
FILING DATE: 02 FEB 1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Thomas C.  
REGISTRATION NUMBER: P-36,989  
REFERENCE/DOCKET NUMBER: 27129/30911  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/346-5750  
TELEFAX: 312/346-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-013-801-2  
  
Query Match 100.0%; Score 943; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 9.9e-70;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CNAFRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQGGTAALQKELKRIKIPDYS 60  
Db 10 CNAFRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQGGTAALQKELKRIKIPDYS 69  
  
Qy 61 DSFKIKHLGKHGHSFYSDMIREFQLPSSQISMPVNVGLKFSISNANIKISGKWKAKRFL 120  
Db 70 DSFKIKHLGKHGHSFYSDMIREFQLPSSQISMPVNVGLKFSISNANIKISGKWKAKRFL 129  
  
Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHLSKSKVGLIQLF 180  
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHLSKSKVGLIQLF 189  
  
Qy 181 HKKI 184  
Db 190 HKKI 193  
  
RESULT 11  
US-08-072-063-2  
Sequence 2, Application US/08072063  
Patent No. 5439807  
GENERAL INFORMATION:  
APPLICANT: Theofan, Georgia  
APPLICANT: Grinna, Lynn S  
APPLICANT: Horwitz, Arnold  
TITLE OF INVENTION: BPI-Immunoglobulin Fusion Proteins  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/072.063



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2005, 11:22:43 ; Search time 47.1759 Seconds  
(without alignments)  
770.608 Million cell updates/sec

Title: US-10-629-516-2  
Perfect score: 2507  
Sequence: 1 MRENARGPCNAPRWVSLMV.....NVVLQPHQNFLLFGADVVK 487

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2507	100.0	487	1 US-08-030-644-2	Sequence 2, Appli
2	2507	100.0	487	1 US-08-013-801-2	Sequence 2, Appli
3	2507	100.0	487	1 US-08-072-063-2	Sequence 2, Appli
4	2507	100.0	487	1 US-08-212-132-2	Sequence 2, Appli
5	2507	100.0	487	1 US-08-414-924-2	Sequence 2, Appli
6	2507	100.0	487	1 US-08-311-611A-69	Sequence 69, Appl
7	2507	100.0	487	1 US-08-311-611A-146	Sequence 146, App
8	2507	100.0	487	1 US-08-173-968-2	Sequence 2, Appli
9	2507	100.0	487	1 US-08-232-527-2	Sequence 2, Appli
10	2507	100.0	487	1 US-08-372-783-69	Sequence 69, Appl
11	2507	100.0	487	1 US-08-372-783-146	Sequence 146, App
12	2507	100.0	487	1 US-08-372-105-69	Sequence 69, Appl
13	2507	100.0	487	1 US-08-372-105-146	Sequence 146, App
14	2507	100.0	487	1 US-08-415-158-2	Sequence 2, Appli
15	2507	100.0	487	1 US-08-064-693-2	Sequence 2, Appli
16	2507	100.0	487	1 US-08-291-113-2	Sequence 2, Appli
17	2507	100.0	487	1 US-08-306-473A-69	Sequence 69, Appl
18	2507	100.0	487	1 US-08-306-473A-146	Sequence 146, App
19	2507	100.0	487	1 US-08-430-417-2	Sequence 2, Appli
20	2507	100.0	487	1 US-08-557-287-2	Sequence 2, Appli
21	2507	100.0	487	1 US-08-470-366-2	Sequence 2, Appli
22	2507	100.0	487	1 US-08-261-660A-12	Sequence 12, Appl
23	2507	100.0	487	1 US-08-209-762-69	Sequence 69, Appl
24	2507	100.0	487	1 US-08-644-290-2	Sequence 2, Appli
25	2507	100.0	487	1 US-08-378-228-2	Sequence 2, Appli
26	2507	100.0	487	1 US-08-927-438-2	Sequence 2, Appli
27	2507	100.0	487	1 US-08-473-344-69	Sequence 69, Appl

28	2507	100.0	487	1 US-08-274-303-2	Sequence 2, Appli
29	2507	100.0	487	1 US-07-915-720D-13	Sequence 13, Appli
30	2507	100.0	487	1 US-08-435-855-2	Sequence 2, Appli
31	2507	100.0	487	2 US-08-466-822-2	Sequence 2, Appli
32	2507	100.0	487	2 US-08-466-624-2	Sequence 2, Appli
33	2507	100.0	487	2 US-08-621-803-265	Sequence 265, App
34	2507	100.0	487	2 US-08-466-826-2	Sequence 2, Appli
35	2507	100.0	487	2 US-08-704-504-2	Sequence 2, Appli
36	2507	100.0	487	2 US-08-485-445A-69	Sequence 69, Appli
37	2507	100.0	487	2 US-08-485-445A-146	Sequence 146, App
38	2507	100.0	487	2 US-08-621-259A-252	Sequence 252, App
39	2507	100.0	487	2 US-08-586-133-2	Sequence 2, Appli
40	2507	100.0	487	2 US-09-063-465-2	Sequence 2, Appli
41	2507	100.0	487	2 US-08-862-785A-2	Sequence 2, Appli
42	2507	100.0	487	2 US-09-081-166-2	Sequence 2, Appli
43	2507	100.0	487	2 US-09-203-159-2	Sequence 2, Appli
44	2507	100.0	487	3 US-09-099-725-2	Sequence 2, Appli
45	2507	100.0	487	3 US-08-756-164-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-08-030-644-2  
; Sequence 2, Application US/08030644  
; Patent No. 5348942  
; GENERAL INFORMATION:  
; APPLICANT: Little, Roger G. II  
; APPLICANT: Gazzano-Santoro, Helene  
; APPLICANT: Parent, James Brian  
; TITLE OF INVENTION: Therapeutic uses of  
; TITLE OF INVENTION: Bactericidal/Permeability-Increasing Protein Products  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/030,644  
; FILING DATE: 19930312  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Shaip, Jeffrey S.  
; REGISTRATION NUMBER: 31,879  
; REFERENCE/DOCKET NUMBER: 31229  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 487 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-030-644-2

Query Match 100.0%; Score 2507; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 6.6e-209;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRENARGPCNAPRWVSLMVVAIGTATTAANPGVVVRISSOKGLDYASQQGTAAQKEL 60  
DB 1 MRENARGPCNAPRWVSLMVVAIGTATTAANPGVVVRISSOKGLDYASQQGTAAQKEL 60

```
QY 61 KRIKIPYDSFKIKHLGKHGHSFYSDIRFQLPSSQISMVNVNGLKFSISNANIKISG 120
DB 61 KRIKIPYDSFKIKHLGKHGHSFYSDIRFQLPSSQISMVNVNGLKFSISNANIKISG 120
QY 121 KWAQKRFLLKMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHISKS 180
DB 121 KWAQKRFLLKMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHISKS 180
QY 181 KVGWLIQLFHKHIESALRNKNSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSIVAGINYL 240
DB 181 KVGWLIQLFHKHIESALRNKNSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSIVAGINYL 240
QY 241 VAPPATTAETLDVQMGGEFYSENHNHPPPPAPPVMEFPAADRMYLGLSDYFNTAGLV 300
DB 241 VAPPATTAETLDVQMGGEFYSENHNHPPPPAPPVMEFPAADRMYLGLSDYFNTAGLV 300
QY 301 YQEAGVLKMTLRDDMIKESKFRLLTKFFGTFLPEVAKFPNNKIQIHVSASTPPHLSVQ 360
DB 301 YQEAGVLKMTLRDDMIKESKFRLLTKFFGTFLPEVAKFPNNKIQIHVSASTPPHLSVQ 360
QY 361 PTGLTTFYPAVDVQAFVLPNSSLASLFLIGHMTTGSMEVSAESNRLVGEKLDRLLELK 420
DB 361 PTGLTTFYPAVDVQAFVLPNSSLASLFLIGHMTTGSMEVSAESNRLVGEKLDRLLELK 420
QY 421 HSNIGPPFVELLDIMNYIVPILVPRVNEKLOKGFPLTPPARVOLYNNVVLQPHQNFLLF 480
DB 421 HSNIGPPFVELLDIMNYIVPILVPRVNEKLOKGFPLTPPARVOLYNNVVLQPHQNFLLF 480
QY 481 GADVYK 487
DB 481 GADVYK 487

RESULT 2
US-08-013-801-2
; Sequence 2, Application US/08013801
; Patent No. 5420019
; GENERAL INFORMATION:
; APPLICANT: Theofan, Georgia
; APPLICANT: Horwitz, Arnold
; APPLICANT: Burke, David
; APPLICANT: Baltain, Manik
; APPLICANT: Grinna, Lynn S
; TITLE OF INVENTION: Stable Bactericidal/Permeability-
; TITLE OF INVENTION: Increasing Protein Products and Pharmaceutical
; TITLE OF INVENTION: Compositions Containing the Same
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/013.801
; FILING DATE: 02 FEB 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 27129/30911
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/346-5750
; TELEFAX: 312/346-9740
; TELEX: 25-3856
```

```
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-013-801-2

Query Match 100.0%; Score 2507; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 6.6e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRENMAAGPCNAPRWVSLMVLVAIGTAVTAAGVNVGVVVRISQKGLDYASQOGTAALQKEL 60
DB 1 MRENMAAGPCNAPRWVSLMVLVAIGTAVTAAGVNVGVVVRISQKGLDYASQOGTAALQKEL 60
QY 61 KRIKIPYDSFKIKHLGKHGHSFYSDIRFQLPSSQISMVNVNGLKFSISNANIKISG 120
DB 61 KRIKIPYDSFKIKHLGKHGHSFYSDIRFQLPSSQISMVNVNGLKFSISNANIKISG 120
QY 121 KWAQKRFLLKMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHISKS 180
DB 121 KWAQKRFLLKMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHISKS 180
QY 181 KVGWLIQLFHKHIESALRNKNSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSIVAGINYL 240
DB 181 KVGWLIQLFHKHIESALRNKNSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSIVAGINYL 240
QY 241 VAPPATTAETLDVQMGGEFYSENHNHPPPPAPPVMEFPAADRMYLGLSDYFNTAGLV 300
DB 241 VAPPATTAETLDVQMGGEFYSENHNHPPPPAPPVMEFPAADRMYLGLSDYFNTAGLV 300
QY 301 YQEAGVLKMTLRDDMIKESKFRLLTKFFGTFLPEVAKFPNNKIQIHVSASTPPHLSVQ 360
DB 301 YQEAGVLKMTLRDDMIKESKFRLLTKFFGTFLPEVAKFPNNKIQIHVSASTPPHLSVQ 360
QY 361 PTGLTTFYPAVDVQAFVLPNSSLASLFLIGHMTTGSMEVSAESNRLVGEKLDRLLELK 420
DB 361 PTGLTTFYPAVDVQAFVLPNSSLASLFLIGHMTTGSMEVSAESNRLVGEKLDRLLELK 420
QY 421 HSNIGPPFVELLDIMNYIVPILVPRVNEKLOKGFPLTPPARVOLYNNVVLQPHQNFLLF 480
DB 421 HSNIGPPFVELLDIMNYIVPILVPRVNEKLOKGFPLTPPARVOLYNNVVLQPHQNFLLF 480
QY 481 GADVYK 487
DB 481 GADVYK 487

RESULT 3
US-08-072-063-2
; Sequence 2, Application US/08072063
; Patent No. 5439807
; GENERAL INFORMATION:
; APPLICANT: Theofan, Georgia
; APPLICANT: Grinna, Lynn S
; APPLICANT: Horwitz, Arnold
; TITLE OF INVENTION: BPI-Immunoglobulin Fusion Proteins
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/072.063
```



```

; FILING DATE: 19930519
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers Thomas C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: 30659
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-072-063-2

Query Match 100.0%; Score 2507; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 6.6e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVWVRIISQKGLDYASQOQTAAQLKEL 60
Db 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVWVRIISQKGLDYASQOQTAAQLKEL 60
Qy 61 KRIKIPDYSDFKIKHLKGHYSPYSMDIREFQLPSSQISMVNPNVGLKFSISNANIKISG 120
Db 61 KRIKIPDYSDFKIKHLKGHYSPYSMDIREFQLPSSQISMVNPNVGLKFSISNANIKISG 120
Qy 121 KWKAQKRLKMSGNFDLSIEGMSISADLKGNSPTSGKPTITCSCSSHINSVHVHISKS 180
Db 121 KWKAQKRLKMSGNFDLSIEGMSISADLKGNSPTSGKPTITCSCSSHINSVHVHISKS 180
Qy 181 KVGWLIQLFHKIESALRNKNSQCEKVTNSVSSKLQPYFQTLPMVTKIDSVAGINYL 240
Db 181 KVGWLIQLFHKIESALRNKNSQCEKVTNSVSSKLQPYFQTLPMVTKIDSVAGINYL 240
Qy 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAADRMVYLGSLDYFFNTAGLV 300
Db 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAADRMVYLGSLDYFFNTAGLV 300
Qy 301 YQEAGVLKMTLRDDMI PKESKFRLLTKFFGTFLPEVAKKFNPMKIQIHVSASTPPHLSVQ 360
Db 301 YQEAGVLKMTLRDDMI PKESKFRLLTKFFGTFLPEVAKKFNPMKIQIHVSASTPPHLSVQ 360
Qy 361 PTGLTFYPADVQAFVLPNSLSASFLIGHMTTGSMEVSAESNRLVGLKLDRLLELK 420
Db 361 PTGLTFYPADVQAFVLPNSLSASFLIGHMTTGSMEVSAESNRLVGLKLDRLLELK 420
Qy 421 HSNIGPPFVELLDIMNYIVPILPRVNEKLGKGFPLPTPARVOLYNNVQLPHQNFLIF 480
Db 421 HSNIGPPFVELLDIMNYIVPILPRVNEKLGKGFPLPTPARVOLYNNVQLPHQNFLIF 480
Qy 481 GADVYK 487
Db 481 GADVYK 487

RESULT 4
US-08-212-132-2
; Sequence 2, Application US/08212132
; Patent No. 547913
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G.
; APPLICANT: Ammons, William Steve
; TITLE OF INVENTION: Therapeutic Uses of Bactericidal/Permeability-
; TITLE OF INVENTION: Increasing Protein Dimer Products
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago

```

```

; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212.132
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/31735
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-212-132-2

Query Match 100.0%; Score 2507; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 6.6e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVWVRIISQKGLDYASQOQTAAQLKEL 60
Db 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVWVRIISQKGLDYASQOQTAAQLKEL 60
Qy 61 KRIKIPDYSDFKIKHLKGHYSPYSMDIREFQLPSSQISMVNPNVGLKFSISNANIKISG 120
Db 61 KRIKIPDYSDFKIKHLKGHYSPYSMDIREFQLPSSQISMVNPNVGLKFSISNANIKISG 120
Qy 121 KWKAQKRLKMSGNFDLSIEGMSISADLKGNSPTSGKPTITCSCSSHINSVHVHISKS 180
Db 121 KWKAQKRLKMSGNFDLSIEGMSISADLKGNSPTSGKPTITCSCSSHINSVHVHISKS 180
Qy 181 KVGWLIQLFHKIESALRNKNSQCEKVTNSVSSKLQPYFQTLPMVTKIDSVAGINYL 240
Db 181 KVGWLIQLFHKIESALRNKNSQCEKVTNSVSSKLQPYFQTLPMVTKIDSVAGINYL 240
Qy 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAADRMVYLGSLDYFFNTAGLV 300
Db 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAADRMVYLGSLDYFFNTAGLV 300
Qy 301 YQEAGVLKMTLRDDMI PKESKFRLLTKFFGTFLPEVAKKFNPMKIQIHVSASTPPHLSVQ 360
Db 301 YQEAGVLKMTLRDDMI PKESKFRLLTKFFGTFLPEVAKKFNPMKIQIHVSASTPPHLSVQ 360
Qy 361 PTGLTFYPADVQAFVLPNSLSASFLIGHMTTGSMEVSAESNRLVGLKLDRLLELK 420
Db 361 PTGLTFYPADVQAFVLPNSLSASFLIGHMTTGSMEVSAESNRLVGLKLDRLLELK 420
Qy 421 HSNIGPPFVELLDIMNYIVPILPRVNEKLGKGFPLPTPARVOLYNNVQLPHQNFLIF 480
Db 421 HSNIGPPFVELLDIMNYIVPILPRVNEKLGKGFPLPTPARVOLYNNVQLPHQNFLIF 480
Qy 481 GADVYK 487
Db 481 GADVYK 487

RESULT 5
US-08-414-924-2
; Sequence 2, Application US/08414924
; Patent No. 5494896

```

GENERAL INFORMATION:  
APPLICANT: Hansbrough, John F.  
TITLE OF INVENTION: Method of Treating Conditions  
TITLE OF INVENTION: Associated With Burn Injuries  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/414,924  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharp, Jeffrey S.  
REGISTRATION NUMBER: 31,879  
REFERENCE/DOCKET NUMBER: 27129/32297  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-414-924-2

Query Match 100.0%; Score 2507; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 6.6e-209;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRENARGPCNAPRWVSLMWLVAGTAVTAANPGVVVRISQKGLDVASQGTAAALQKEL 60  
Db 1 MRENARGPCNAPRWVSLMWLVAGTAVTAANPGVVVRISQKGLDVASQGTAAALQKEL 60  
Qy 61 KRKIPDYSDFKIKHLGKHGHSFYSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISG 120  
Db 61 KRKIPDYSDFKIKHLGKHGHSFYSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISG 120  
Qy 121 KWKAQKRFLLKMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKS 180  
Db 121 KWKAQKRFLLKMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKS 180  
Qy 181 KVGWLIQLFHKIKIESALRNKNSOVCEKVTNSVSKLPYFOTLPVMTKIDSVAGINYL 240  
Db 181 KVGWLIQLFHKIKIESALRNKNSOVCEKVTNSVSKLPYFOTLPVMTKIDSVAGINYL 240  
Qy 241 VAPPATTAETLDVQMKGEFFYSNHNPPPPAPPVMEFPAAHDMVYLGSLDYFFENTAGLV 300  
Db 241 VAPPATTAETLDVQMKGEFFYSNHNPPPPAPPVMEFPAAHDMVYLGSLDYFFENTAGLV 300  
Qy 301 YQEAGVLKWTLRDDMI PKESKFRITTKTFGTFLEVAKKPNNMKIQIHVSASTPPHLSVQ 360  
Db 301 YQEAGVLKWTLRDDMI PKESKFRITTKTFGTFLEVAKKPNNMKIQIHVSASTPPHLSVQ 360  
Qy 361 PTGLTFTFPAVDVQFAVLPNSSLASLFLIGHMTTGSMEVSAESNRLVGELKLDRLLELK 420  
Db 361 PTGLTFTFPAVDVQFAVLPNSSLASLFLIGHMTTGSMEVSAESNRLVGELKLDRLLELK 420  
Qy 421 HSNIGPPFVELLDQIMNYIVPILVPRVNEKIQKGFPLPTPARVOLYNNVLPQHONFLF 480  
Db 421 HSNIGPPFVELLDQIMNYIVPILVPRVNEKIQKGFPLPTPARVOLYNNVLPQHONFLF 480

Qy 481 GADVVK 487  
Db 481 GADVVK 487  
RESULT 6  
US-08-311-611A-69  
Sequence 69, Application US/08311611A  
Patent No. 5523288  
GENERAL INFORMATION:  
APPLICANT: Cohen, Jonathan  
APPLICANT: Kung, Ada H.C.  
APPLICANT: Lambert, Jr., Lewis H.  
TITLE OF INVENTION: Method for Treating Gram-Negative Bacterial  
TITLE OF INVENTION: Infection by Administration of  
TITLE OF INVENTION: Bactericidal/Permeability-Increasing  
TITLE OF INVENTION:  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM: disk  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/311,611A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/273,401  
FILING DATE: 11-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/125,651  
FILING DATE: 22-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharp, Jeffrey S.  
REGISTRATION/DOCKET NUMBER: 31,879  
REFERENCE/DOCKET NUMBER: 32251  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: "rBPI"  
US-08-311-611A-69

Query Match 100.0%; Score 2507; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 6.6e-209;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRENARGPCNAPRWVSLMWLVAGTAVTAANPGVVVRISQKGLDVASQGTAAALQKEL 60  
Db 1 MRENARGPCNAPRWVSLMWLVAGTAVTAANPGVVVRISQKGLDVASQGTAAALQKEL 60  
Qy 61 KRKIPDYSDFKIKHLGKHGHSFYSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISG 120  
Db 61 KRKIPDYSDFKIKHLGKHGHSFYSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISG 120  
Qy 121 KWKAQKRFLLKMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKS 180  
Db 121 KWKAQKRFLLKMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKS 180

Db 121 KWKAQKRLKMSGNFDLSIEGMSISADLKLGNSPTSGKPTITCSCSSHINSVHVHISKS 180  
Qy 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLOPYFQTLPMVTKIDSVAGINYL 240  
Db 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLOPYFQTLPMVTKIDSVAGINYL 240  
Qy 241 VAPPATTAETLDVQMKGFYSNNHNPFPFAPPVMEFFAAHDMVYLGSDYFFNTAGLV 300  
Db 241 VAPPATTAETLDVQMKGFYSNNHNPFPFAPPVMEFFAAHDMVYLGSDYFFNTAGLV 300  
Qy 301 YOEAGVLKMTLRDDMI PKESKRLTTKFGTFLPEVAKKFNPKIQIHVSASTPPHLSVQ 360  
Db 301 YOEAGVLKMTLRDDMI PKESKRLTTKFGTFLPEVAKKFNPKIQIHVSASTPPHLSVQ 360  
Qy 361 PTGLTFYPAVDVQAFVLPNSSLASFLIGHMTTSGMEVSAESNRLVGLKLDRLLELK 420  
Db 361 PTGLTFYPAVDVQAFVLPNSSLASFLIGHMTTSGMEVSAESNRLVGLKLDRLLELK 420  
Qy 421 HSNIGPPFVELLDIMNVIIVPLVLPVNEKLOKGFPLTPARVOLYNNVLOPHQNFLLF 480  
Db 421 HSNIGPPFVELLDIMNVIIVPLVLPVNEKLOKGFPLTPARVOLYNNVLOPHQNFLLF 480  
Qy 481 GADVYK 487  
Db 481 GADVYK 487

RESULT 7

US-08-311-611A-146  
; Sequence 146, Application US/08311611A  
; Patent No. 5523288  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Jonathan  
; APPLICANT: Kung, Ada H.C.  
; APPLICANT: Lambert, Jr., Lewis H.  
; TITLE OF INVENTION: Method for Treating Gram-Negative Bacterial  
; TITLE OF INVENTION: Infection by Administration of  
; TITLE OF INVENTION: Bactericidal/Permeability-Increasing  
; TITLE OF INVENTION:  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/311,611A  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/273,401  
; FILING DATE: 11-JUL-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/125,651  
; FILING DATE: 22-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Shaip, Jeffrey S.  
; REGISTRATION NUMBER: 31,879  
; REFERENCE/DOCKET NUMBER: 32251  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 146:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 487 amino acids  
; TYPE: amino acid

; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-311-611A-146  
Query Match 100.0%; Score 2507; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 6.6e-209; Indels 0; Gaps 0;  
Matches 487; Conservative 0; Mismatches 0;  
Qy 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAAVPGVVVRIISQKGLDYASQQTAAQLKEL 60  
Db 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAAVPGVVVRIISQKGLDYASQQTAAQLKEL 60  
Qy 61 KRIKIPDYSDFPKIKHLGKGHYFSYMDIRFQLPSSQISMPVNVGLKFSISNAIKISG 120  
Db 61 KRIKIPDYSDFPKIKHLGKGHYFSYMDIRFQLPSSQISMPVNVGLKFSISNAIKISG 120  
Qy 121 KWKAQKRLKMSGNFDLSIEGMSISADLKLGNSPTSGKPTITCSCSSHINSVHVHISKS 180  
Db 121 KWKAQKRLKMSGNFDLSIEGMSISADLKLGNSPTSGKPTITCSCSSHINSVHVHISKS 180  
Qy 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLOPYFQTLPMVTKIDSVAGINYL 240  
Db 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLOPYFQTLPMVTKIDSVAGINYL 240  
Qy 241 VAPPATTAETLDVQMKGFYSNNHNPFPFAPPVMEFFAAHDMVYLGSDYFFNTAGLV 300  
Db 241 VAPPATTAETLDVQMKGFYSNNHNPFPFAPPVMEFFAAHDMVYLGSDYFFNTAGLV 300  
Qy 301 YOEAGVLKMTLRDDMI PKESKRLTTKFGTFLPEVAKKFNPKIQIHVSASTPPHLSVQ 360  
Db 301 YOEAGVLKMTLRDDMI PKESKRLTTKFGTFLPEVAKKFNPKIQIHVSASTPPHLSVQ 360  
Qy 361 PTGLTFYPAVDVQAFVLPNSSLASFLIGHMTTSGMEVSAESNRLVGLKLDRLLELK 420  
Db 361 PTGLTFYPAVDVQAFVLPNSSLASFLIGHMTTSGMEVSAESNRLVGLKLDRLLELK 420  
Qy 421 HSNIGPPFVELLDIMNVIIVPLVLPVNEKLOKGFPLTPARVOLYNNVLOPHQNFLLF 480  
Db 421 HSNIGPPFVELLDIMNVIIVPLVLPVNEKLOKGFPLTPARVOLYNNVLOPHQNFLLF 480  
Qy 481 GADVYK 487  
Db 481 GADVYK 487

RESULT 8

US-08-173-968-2  
; Sequence 2, Application US/08173968  
; Patent No. 5576292  
; GENERAL INFORMATION:  
; APPLICANT: Elsbach, Peter  
; APPLICANT: Weiss, Jerrold  
; TITLE OF INVENTION: Biologically Active  
; TITLE OF INVENTION: Bactericidal/Permeability-Increasing Protein Fragments  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howard M. Frankfort  
; STREET: 805 Third Ave.  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/173,968  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/754,204

```
; FILING DATE: 26-AUG-1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Frankfort, Howard M.
; REGISTRATION NUMBER: 32,613
; REFERENCE/DOCKET NUMBER: 5969/05982US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: blood
; CELL TYPE: promyelocytic leukemia cells
; US-08-173-968-2
```

```
Query Match 100.0%; Score 2507; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 6.6e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQGGTAALQKEL 60
DB 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQGGTAALQKEL 60

QY 61 KRIPIDYDSFKIKHLGKGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISG 120
DB 61 KRIPIDYDSFKIKHLGKGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISG 120

QY 121 KWAKQKFLKWSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180
DB 121 KWAKQKFLKWSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180

QY 181 KVGHLIQLFHKKIESALRNKNQNSQVCEKVTNSVSSKLQPYFOTLPVMTKIDSVAGINYL 240
DB 181 KVGHLIQLFHKKIESALRNKNQNSQVCEKVTNSVSSKLQPYFOTLPVMTKIDSVAGINYL 240

QY 241 VAPPATTAETLDVQMGGEFYSENHNPPPPAPPVMEFPAAHDMRVYLGLSDYFNTAGLV 300
DB 241 VAPPATTAETLDVQMGGEFYSENHNPPPPAPPVMEFPAAHDMRVYLGLSDYFNTAGLV 300

QY 301 YQEAGVLKMTLRDDMI PKESKFRLLTKFFGTFLPEVAKFPNMKIQIHVSASTPPHLSVQ 360
DB 301 YQEAGVLKMTLRDDMI PKESKFRLLTKFFGTFLPEVAKFPNMKIQIHVSASTPPHLSVQ 360

QY 361 PTGLTFFPAVDVQAFVLPNSLSASFLIGHMTTGSMEVSAESNRLVGELKLDRLLELK 420
DB 361 PTGLTFFPAVDVQAFVLPNSLSASFLIGHMTTGSMEVSAESNRLVGELKLDRLLELK 420

QY 421 HSNIGPPFVELLDIMNYIVPILVLRVNEKLOKGFPLPTPARVOLNVVLPQHONFLFF 480
DB 421 HSNIGPPFVELLDIMNYIVPILVLRVNEKLOKGFPLPTPARVOLNVVLPQHONFLFF 480

QY 481 GADVYK 487
DB 481 GADVYK 487
```

```
RESULT 9
US-08-232-527-2
; Sequence 2, Application US/08232527
; Patent No. 5578568
; GENERAL INFORMATION:
; APPLICANT: Ammons, William Steve et al.
; TITLE OF INVENTION: Method of Treating Conditions Associated with
; Intestinal Ischemia/Reperfusion
```

```
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,527
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/32043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-232-527-2
```

```
Query Match 100.0%; Score 2507; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 6.6e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQGGTAALQKEL 60
DB 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQGGTAALQKEL 60

QY 61 KRIPIDYDSFKIKHLGKGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISG 120
DB 61 KRIPIDYDSFKIKHLGKGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISG 120

QY 121 KWAKQKFLKWSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180
DB 121 KWAKQKFLKWSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180

QY 181 KVGHLIQLFHKKIESALRNKNQNSQVCEKVTNSVSSKLQPYFOTLPVMTKIDSVAGINYL 240
DB 181 KVGHLIQLFHKKIESALRNKNQNSQVCEKVTNSVSSKLQPYFOTLPVMTKIDSVAGINYL 240

QY 241 VAPPATTAETLDVQMGGEFYSENHNPPPPAPPVMEFPAAHDMRVYLGLSDYFNTAGLV 300
DB 241 VAPPATTAETLDVQMGGEFYSENHNPPPPAPPVMEFPAAHDMRVYLGLSDYFNTAGLV 300

QY 301 YQEAGVLKMTLRDDMI PKESKFRLLTKFFGTFLPEVAKFPNMKIQIHVSASTPPHLSVQ 360
DB 301 YQEAGVLKMTLRDDMI PKESKFRLLTKFFGTFLPEVAKFPNMKIQIHVSASTPPHLSVQ 360

QY 361 PTGLTFFPAVDVQAFVLPNSLSASFLIGHMTTGSMEVSAESNRLVGELKLDRLLELK 420
DB 361 PTGLTFFPAVDVQAFVLPNSLSASFLIGHMTTGSMEVSAESNRLVGELKLDRLLELK 420

QY 421 HSNIGPPFVELLDIMNYIVPILVLRVNEKLOKGFPLPTPARVOLNVVLPQHONFLFF 480
DB 421 HSNIGPPFVELLDIMNYIVPILVLRVNEKLOKGFPLPTPARVOLNVVLPQHONFLFF 480

QY 481 GADVYK 487
DB 481 GADVYK 487
```

```

RESULT 10
US-08-372-783-69
; Sequence 69, Application US/08372783
; Patent No. 5578572
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Arnold H.
; APPLICANT: Lambert, Lewis H.
; APPLICANT: Little, Roger G.
; TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and
; TITLE OF INVENTION: Materials
; NUMBER OF SEQUENCES: 237
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/372,783
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/32415
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; NAME/KEY: misc_feature
; OTHER INFORMATION: "rBPI"
US-08-372-783-69

Query Match 100.0%; Score 2507; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 6.6e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAAVNFPGVVVRIISQKGLDYASQQGTAALQKEL 60
Db 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAAVNFPGVVVRIISQKGLDYASQQGTAALQKEL 60

Qy 61 KRIKIPDYSDFKIKHLKGHSYFSDMDIRFQLPSSQISMVNPVGLKFSINANIKISG 120
Db 61 KRIKIPDYSDFKIKHLKGHSYFSDMDIRFQLPSSQISMVNPVGLKFSINANIKISG 120

Qy 121 KWKAKQKRLKWSGNFDLIEGWSISADLKLGSNPTSGKPTITCSCSHINSVHVHISKS 180
Db 121 KWKAKQKRLKWSGNFDLIEGWSISADLKLGSNPTSGKPTITCSCSHINSVHVHISKS 180

Qy 181 KVGWLIQLFHKKIESALRNKNNSQVCEKVTNSVSKLPQYFQTLPVMTKIDS VAGIN YGL 240
Db 181 KVGWLIQLFHKKIESALRNKNNSQVCEKVTNSVSKLPQYFQTLPVMTKIDS VAGIN YGL 240

Db 181 KVGWLIQLFHKKIESALRNKNNSQVCEKVTNSVSKLPQYFQTLPVMTKIDS VAGIN YGL 240
Qy 241 VAPPATTAETLDVQMKGEFYSENHNPPFPAPPVMEFPAAHADRMYVLGLSDYFFNTAGLV 300
Db 241 VAPPATTAETLDVQMKGEFYSENHNPPFPAPPVMEFPAAHADRMYVLGLSDYFFNTAGLV 300
Qy 301 YQEAGVLKMTLRDDMIPIKESKFRLTTFKFGFTFLPEVAKKPPNMKIQIHVSASTPPHLSVQ 360
Db 301 YQEAGVLKMTLRDDMIPIKESKFRLTTFKFGFTFLPEVAKKPPNMKIQIHVSASTPPHLSVQ 360
Qy 361 PTGLTFYPAVDVQAFVLPNSSLASLFLIGHHTTGSMEVSAESNRLVCELKLDRLLELK 420
Db 361 PTGLTFYPAVDVQAFVLPNSSLASLFLIGHHTTGSMEVSAESNRLVCELKLDRLLELK 420
Qy 421 HSNIGPPFVELLQDIMNYIIVPLVLRVNEKLGKGFPLPTPARVQLYNNVVLQPHQNFLLF 480
Db 421 HSNIGPPFVELLQDIMNYIIVPLVLRVNEKLGKGFPLPTPARVQLYNNVVLQPHQNFLLF 480
Qy 481 GADVYK 487
Db 481 GADVYK 487

RESULT 11
US-08-372-783-146
; Sequence 146, Application US/08372783
; Patent No. 5578572
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Arnold H.
; APPLICANT: Lambert, Lewis H.
; APPLICANT: Little, Roger G.
; TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and
; TITLE OF INVENTION: Materials
; NUMBER OF SEQUENCES: 237
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/372,783
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/32415
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 146:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; NAME/KEY: protein
; OTHER INFORMATION: "rBPI"
US-08-372-783-146
```

```
Query Match      100.0%; Score 2507; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 6.6e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPVGWVVRISQKGLDYASQGGTAALQKEL 60
DB 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPVGWVVRISQKGLDYASQGGTAALQKEL 60

QY 61 KRKIPDYSDFKIKHLGKHGHSFYSDMIREFQLPSSQISMPVNVGLKFSISNANIKISG 120
DB 61 KRKIPDYSDFKIKHLGKHGHSFYSDMIREFQLPSSQISMPVNVGLKFSISNANIKISG 120

QY 121 KWAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180
DB 121 KWAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180

QY 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240
DB 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240

QY 241 VAPPATTAETLDVQMGGEFYSENHNPPPPAPPVMEFPAAHDMVYLGSLDYFFNTAGLV 300
DB 241 VAPPATTAETLDVQMGGEFYSENHNPPPPAPPVMEFPAAHDMVYLGSLDYFFNTAGLV 300

QY 301 YQAGVLMKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQ 360
DB 301 YQAGVLMKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQ 360

QY 361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKDRLLLELK 420
DB 361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKDRLLLELK 420

QY 421 HSNIGPPVVELLDQIMNYIVPILVPRVNEKLGKGFPLTPPARVQLYNVVYLPQHONFLFP 480
DB 421 HSNIGPPVVELLDQIMNYIVPILVPRVNEKLGKGFPLTPPARVQLYNVVYLPQHONFLFP 480

QY 481 GADVYK 487
DB 481 GADVYK 487

RESULT 12
US-08-372-105-69
; Sequence 69, Application US/08372105
; Patent No. 5627153
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G.
; APPLICANT: Lim, Edward
; APPLICANT: Lambert, Lewis H.
; APPLICANT: Scannon, Patrick J.
; TITLE OF INVENTION: Anti-Fungal Materials and Methods
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/372,105
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
```

```
; FILING DATE: 11-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/32415
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "rBPI"
; US-08-372-105-69

Query Match      100.0%; Score 2507; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 6.6e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPVGWVVRISQKGLDYASQGGTAALQKEL 60
DB 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPVGWVVRISQKGLDYASQGGTAALQKEL 60

QY 61 KRKIPDYSDFKIKHLGKHGHSFYSDMIREFQLPSSQISMPVNVGLKFSISNANIKISG 120
DB 61 KRKIPDYSDFKIKHLGKHGHSFYSDMIREFQLPSSQISMPVNVGLKFSISNANIKISG 120

QY 121 KWAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180
DB 121 KWAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180

QY 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240
DB 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240

QY 241 VAPPATTAETLDVQMGGEFYSENHNPPPPAPPVMEFPAAHDMVYLGSLDYFFNTAGLV 300
DB 241 VAPPATTAETLDVQMGGEFYSENHNPPPPAPPVMEFPAAHDMVYLGSLDYFFNTAGLV 300

QY 301 YQAGVLMKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQ 360
DB 301 YQAGVLMKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQ 360

QY 361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKDRLLLELK 420
DB 361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKDRLLLELK 420

QY 421 HSNIGPPVVELLDQIMNYIVPILVPRVNEKLGKGFPLTPPARVQLYNVVYLPQHONFLFP 480
DB 421 HSNIGPPVVELLDQIMNYIVPILVPRVNEKLGKGFPLTPPARVQLYNVVYLPQHONFLFP 480

QY 481 GADVYK 487
DB 481 GADVYK 487

RESULT 13
US-08-372-105-146
; Sequence 146, Application US/08372105
; Patent No. 5627153
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G.
; APPLICANT: Lim, Edward
; APPLICANT: Lambert, Lewis H.
; APPLICANT: Scannon, Patrick J.
```

TITLE OF INVENTION: Anti-Fungal Materials and Methods  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/372,105

FILING DATE: 11-JUL-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/273,540  
FILING DATE: 11-JUL-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/209,762  
FILING DATE: 11-MAR-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/183,222  
FILING DATE: 14-JAN-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Rin-Laures Li-Hsien  
REGISTRATION NUMBER: 33,547  
REFERENCE/DOCKET NUMBER: 27129/32415

TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 146:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-372-105-146

Query Match 100.0%; Score 2507; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 6.6e-209;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRIISQKGLDYASQQGTAALQKEL 60  
Db 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRIISQKGLDYASQQGTAALQKEL 60  
Qy 61 KRKIPDYSDSKIKHLGKHGHSYFSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISG 120  
Db 61 KRKIPDYSDSKIKHLGKHGHSYFSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISG 120  
Qy 121 KWKAKQKRLKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKS 180  
Db 121 KWKAKQKRLKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKS 180  
Qy 181 KVGWLIQLFHKKIESALRNKMSQCEKVTNSVSSKLOPYFQTLVPMTKIDSVAGINYL 240  
Db 181 KVGWLIQLFHKKIESALRNKMSQCEKVTNSVSSKLOPYFQTLVPMTKIDSVAGINYL 240  
Qy 241 VAPPATTATETLDVQMGFEYSNHNPPFPVMEFFPAADHDMVYGLSDYFFNTAGLV 300  
Db 241 VAPPATTATETLDVQMGFEYSNHNPPFPVMEFFPAADHDMVYGLSDYFFNTAGLV 300  
Qy 301 YQEAGLVKMTLRDDMIKPKESKRLATTKPFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360  
Db 301 YQEAGLVKMTLRDDMIKPKESKRLATTKPFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360  
Qy 361 PTGLTFYPAVDVQAFVLPNSLASLFLIGMTTGSMEVSAESNRLVGELKLDRLLELK 420  
Db 361 PTGLTFYPAVDVQAFVLPNSLASLFLIGMTTGSMEVSAESNRLVGELKLDRLLELK 420

Qy 421 HSNIGPFPVELLDIMNVIYPILVLPVNEKLGKGFPLPTPARVOLXNVVLQPHQNFLLF 480  
Db 421 HSNIGPFPVELLDIMNVIYPILVLPVNEKLGKGFPLPTPARVOLXNVVLQPHQNFLLF 480  
Qy 481 GADVYK 487  
Db 481 GADVYK 487

## RESULT 14

US-08-415-158-2  
Sequence 2, Application US/08415158  
Patent No. 5639727

GENERAL INFORMATION:  
APPLICANT: Little, Roger G. II  
APPLICANT: Gazzano-Santoro, Helene  
APPLICANT: Parent, James Brian

TITLE OF INVENTION: Therapeutic uses of  
Bactericidal/Permeability-Increasing Protein Products

NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/415,158  
FILING DATE: 12-MAR-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08/093,202  
FILING DATE: 12-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharp, Jeffrey S.  
REGISTRATION NUMBER: 31,879  
REFERENCE/DOCKET NUMBER: 31580  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-415-158-2

Query Match 100.0%; Score 2507; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 6.6e-209;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRIISQKGLDYASQQGTAALQKEL 60  
Db 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRIISQKGLDYASQQGTAALQKEL 60  
Qy 61 KRKIPDYSDSKIKHLGKHGHSYFSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISG 120  
Db 61 KRKIPDYSDSKIKHLGKHGHSYFSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISG 120  
Qy 121 KWKAKQKRLKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKS 180  
Db 121 KWKAKQKRLKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKS 180



QY 181 KVGWLIQLFHKHTESALRNKMSOVCEKVTNSVSSKLPQYFOTLPVMTKIDS VAGIN YGL 240  
DB 181 KVGWLIQLFHKHTESALRNKMSOVCEKVTNSVSSKLPQYFOTLPVMTKIDS VAGIN YGL 240  
QY 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAADRMVYLGLSDYFNTAGLV 300  
DB 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAADRMVYLGLSDYFNTAGLV 300  
QY 301 YQAGVLKMTLRDDMIPEKSKFRLTTKFFGTFLPEVAKFPNNMKIQIHVSASTPPHLSVQ 360  
DB 301 YQAGVLKMTLRDDMIPEKSKFRLTTKFFGTFLPEVAKFPNNMKIQIHVSASTPPHLSVQ 360  
QY 361 PTGLTFYPADVQAFVLPNSSLASLFLIGHHTTGSMEVSAESNRLVGLKLDRLLELK 420  
DB 361 PTGLTFYPADVQAFVLPNSSLASLFLIGHHTTGSMEVSAESNRLVGLKLDRLLELK 420  
QY 421 HSNIGPPFVELLDQIMNYIVPILVPRVNEKLOKGFPLPTPARVOLYNNVVLQPHQNPLLF 480  
DB 421 HSNIGPPFVELLDQIMNYIVPILVPRVNEKLOKGFPLPTPARVOLYNNVVLQPHQNPLLF 480  
QY 481 GADVYK 487  
DB 481 GADVYK 487

## RESULT 15

US-08-064-693-2  
; Sequence 2, Application US/08064693  
; Patent No. 5643570  
; GENERAL INFORMATION:  
; APPLICANT: Theofan, Georgia  
; APPLICANT: Grinna, Lynn S  
; APPLICANT: Horwitz, Arnold  
; TITLE OF INVENTION: BPI-Immunoglobulin Fusion Proteins  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Borun  
; STREET: 6300 Sears Tower, 233 South Wacker  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/064,693  
; FILING DATE: 19930519  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers Thomas C.  
; REGISTRATION NUMBER: 36,989  
; REFERENCE/DOCKET NUMBER: 30659  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 487 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-064-693-2

Query Match 100.0%; Score 2507; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 6.6e-209;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRENMARGPCNAPRWVSLMVLVAIGTAVTAANNPVGWVVRISQKGLDYASOQGTAAQLKEL 60  
DB 1 MRENMARGPCNAPRWVSLMVLVAIGTAVTAANNPVGWVVRISQKGLDYASOQGTAAQLKEL 60  
QY 61 KRIRIPDYSDFKIKHLGKHGHSFYSDIREFQLPSSQISWVNVNGLKFSISNANIKISG 120  
DB 61 KRIRIPDYSDFKIKHLGKHGHSFYSDIREFQLPSSQISWVNVNGLKFSISNANIKISG 120  
QY 121 KWKAQKRFKMSGNFPLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKS 180  
DB 121 KWKAQKRFKMSGNFPLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKS 180  
QY 181 KVGWLIQLFHKHTESALRNKMSOVCEKVTNSVSSKLPQYFOTLPVMTKIDS VAGIN YGL 240  
DB 181 KVGWLIQLFHKHTESALRNKMSOVCEKVTNSVSSKLPQYFOTLPVMTKIDS VAGIN YGL 240  
QY 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAADRMVYLGLSDYFNTAGLV 300  
DB 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAADRMVYLGLSDYFNTAGLV 300  
QY 301 YQAGVLKMTLRDDMIPEKSKFRLTTKFFGTFLPEVAKFPNNMKIQIHVSASTPPHLSVQ 360  
DB 301 YQAGVLKMTLRDDMIPEKSKFRLTTKFFGTFLPEVAKFPNNMKIQIHVSASTPPHLSVQ 360  
QY 361 PTGLTFYPADVQAFVLPNSSLASLFLIGHHTTGSMEVSAESNRLVGLKLDRLLELK 420  
DB 361 PTGLTFYPADVQAFVLPNSSLASLFLIGHHTTGSMEVSAESNRLVGLKLDRLLELK 420  
QY 421 HSNIGPPFVELLDQIMNYIVPILVPRVNEKLOKGFPLPTPARVOLYNNVVLQPHQNPLLF 480  
DB 421 HSNIGPPFVELLDQIMNYIVPILVPRVNEKLOKGFPLPTPARVOLYNNVVLQPHQNPLLF 480  
QY 481 GADVYK 487  
DB 481 GADVYK 487

Search completed: October 21, 2005, 11:32:57  
Job time : 49.1759 secs



Res 1 + full length  
check for  
res. part.

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2005, 11:22:38 ; Search time 64.4411 Seconds  
(without alignments)  
1104.324 Million cell updates/sec

Title: US-10-629-516-2\_COPY\_10\_193

Perfect score: 943  
Sequence: 1 CNAPRWSLMVLVAIGTAVT.....HVHISKVGVGLQLFHKI 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	943	100.0	220	2 AAR88746	rBPI(1-193)
2	943	100.0	221	2 AAW16801	Recombinant
3	943	100.0	230	2 AAW16800	Recombinant
4	943	100.0	230	2 AAW47091	Human rec.
5	943	100.0	243	2 AAR33777	rBPI from
6	943	100.0	243	2 AAW16803	Recombinant
7	943	100.0	267	2 AAW16802	Recombinant
8	943	100.0	300	2 AAW62410	Recombinant
9	943	100.0	368	2 AAR21840	Human 57k
10	943	100.0	368	2 AAR71291	Human bac
11	943	100.0	483	4 AAB66058	Human bac
12	943	100.0	483	6 ABO32712	Secreted
13	943	100.0	483	6 ABU04504	Human exp
14	943	100.0	483	6 ABU04575	Human exp
15	943	100.0	483	8 ADQ10386	Human pol
16	943	100.0	483	8 ADQ98258	Human pol
17	943	100.0	487	1 AAU06198	Human bac
18	943	100.0	487	2 AAR24777	Sequence
19	943	100.0	487	2 AAR44420	PING4512
20	943	100.0	487	2 AAR43886	Human bac
21	943	100.0	487	2 AAR62370	Recombinant
22	943	100.0	487	2 AAR57901	Bacterici
23	943	100.0	487	2 AAR62344	Recombinant
24	943	100.0	487	2 AAR68923	Bacterici
25	943	100.0	487	2 AAR71290	Human bac

26	943	100.0	487	2 AAR79185	Recombinant
27	943	100.0	487	2 AAR79021	Bacterici
28	943	100.0	487	2 AAR81247	Recombinant
29	943	100.0	487	2 AAR81245	Bacterici
30	943	100.0	487	2 AAR80995	Bacterici
31	943	100.0	487	2 AAR67998	Holoprote
32	943	100.0	487	2 AAR86455	rBPI for
33	943	100.0	487	2 AAR76243	Recombinant
34	943	100.0	487	2 AAW05852	Recombinant
35	943	100.0	487	2 AAW16796	Recombinant
36	943	100.0	487	2 AAW16816	Recombinant
37	943	100.0	487	2 AAW16797	Recombinant
38	943	100.0	487	2 AAW16798	Recombinant
39	943	100.0	487	2 AAR97568	Human bac
40	943	100.0	487	2 AAW17987	Bacterici
41	943	100.0	487	2 AAW44650	Human bac
42	943	100.0	487	2 AAW01702	Human bac
43	943	100.0	487	2 AAW17986	Human bac
44	943	100.0	487	2 AAW47090	Human bac
45	943	100.0	487	2 AAW40141	Human rec

ALIGNMENTS

RESULT 1  
AAR88746  
ID AAR88746 standard; protein; 220 AA.  
AC AAR88746;  
XX  
DT 10-APR-1996 (first entry)  
DE rBPI(1-193) with 27 amino acid signal peptide.  
XX  
KW bactericidal-permeability increasing protein; BPI; truncated; dimer;  
KW endotoxic shock; heparin neutralisation; angiogenesis; inhibitor; sb.  
XX  
OS Synthetic.  
XX  
FH Key  
FT Peptide  
FT /label= signal  
FT /note= "the first 4 amino acids of the native signal  
FT peptide have been deleted"  
FT 28..220  
FT Protein  
FT /label= rBPI(1-193)  
FT /note= "the first 193 residues of human mature BPI"

US5447913-A.  
05-SEP-1995.  
11-MAR-1994; 94US-00212132.  
11-MAR-1994; 94US-00212132.  
(XOMA ) XOMA CORP.  
Ammons WS, Little RG;  
WPI; 1995-319904/41.  
Improved use of a bactericidal-permeability increasing protein - for  
neutralisation of heparin and treatment of endotoxaemia, by admin. as  
covalently linked dimer of N-terminal fragment.  
Example 1; Page 2; 36pp; English.  
Compositions of N-terminal fragments (i.e. amino acids 1-193 to 1-199) of  
human bactericidal-permeability increasing (BPI) protein are used to  
neutralise heparin and to treat endotoxaemia. Efficacy of such compans.  
is improved when they comprise at least 50% of the truncated rBPI in

CC dimeric form. The present sequence is that of rBPI(1-193) in which the  
 CC first 4 amino acids of the BPI signal peptide are removed; the codon  
 CC specifying the fifth amino acid of the signal sequence (Met at position -  
 CC 27) is placed in the context of a consensus Kozak translation initiation  
 CC sequence. This truncated rBPI is the preferred monomer for dimerisation  
 CC in the presence of copper 2+ ions. N.B. The patent specification includes  
 CC the known full-length BPI sequence but does not contain sequences for any  
 CC of the truncated versions of the protein. The present sequence has been  
 CC obtained by modifying the wild-type sequence according to the description  
 CC given by the inventors  
 XX  
 SQ Sequence 220 AA;

Query Match 100.0%; Score 943; DB 2; Length 220;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-92;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQQTAAALQKELKRIKIPDYS 60  
 DB 6 CNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQQTAAALQKELKRIKIPDYS 65  
 QY 61 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMPVNVGLKFSISNANIKISGKWKAKQKRF 120  
 DB 66 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMPVNVGLKFSISNANIKISGKWKAKQKRF 125  
 QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKSKVGLIQLF 180  
 DB 126 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKSKVGLIQLF 185  
 QY 181 HKKI 184  
 DB 186 HKKI 189

RESULT 2  
 ID AAW16801 standard; protein; 221 AA.  
 XX AAW16801;  
 XX 28-JUL-1997 (first entry)  
 DT Recombinant endotoxin neutralising polypeptide Lot #159699.  
 DE  
 XX Recombinant; endotoxin; neutralisation; RNP; Lot #159699;  
 KW lipopolysaccharide; LPS; bactericidal; permeability; increase; BPI;  
 KW detection; Gram-negative; bacterium; infection; prevention; treatment;  
 KW disorder; mediation; stimulation; neutrophil; mononuclear cell;  
 KW inhibition; shock; anemia; anaemia;  
 KW disseminated intravascular coagulation; thrombocytopenia;  
 KW thrombocytopenia; adult respiratory distress syndrome; ARDS;  
 KW renal failure; liver disease; half life; human.  
 XX Homo sapiens.  
 OS Synthetic.

XX Key Location/Qualifiers  
 PH Peptide 1. .31  
 FT /label= sig\_peptide  
 FT  
 PN WO9634873-A1.  
 XX  
 XX 07-NOV-1996.  
 PD  
 XX 01-MAY-1996; 96WO-US006134.  
 XX  
 XX 01-MAY-1995; 95US-00431517.  
 PR  
 XX (INCY-) INCYTE PHARM INC.  
 PA  
 XX Scott RW, Marra MN;  
 PI  
 XX WPI; 1996-506090/50.  
 XX  
 DR

XX Lipo:polysaccharide binding and endotoxin neutralising polypeptide -  
 PT useful in diagnosis, prevention and treatment of Gram-negative bacterial  
 PT infection and associated disorders and conditions.  
 XX  
 PS Example 1; Page: 147pp; English.

XX The present sequence is the recombinant endotoxin neutralising  
 CC polypeptide (RNP) B(1-190) (Lot #159699), which comprises residues 1-190  
 CC of human bactericidal/permeability increasing protein (hBPI). The RNP,  
 CC which selectively and specifically binds lipopolysaccharide (LPS) and has  
 CC endotoxin neutralising activity, can be used to detect a site of Gram  
 CC negative bacterial infection, and prevent or treat endotoxin related  
 CC disorders, preferably where LPS mediated stimulation of neutrophils and  
 CC mononuclear cells is inhibited, e.g. shock, disseminated intravascular  
 CC coagulation, anaemia, thrombocytopenia, adult respiratory distress  
 CC syndrome, renal failure, liver disease and conditions associated with  
 CC Gram negative bacterial infection. The RNP has an enhanced serum half  
 CC life relative to naturally occurring BPI, and binds LPS without  
 CC triggering a significant, undesirable immune response. N.B. Sequence not  
 CC given in specification, but produced using the wild type hBPI sequence  
 CC given in figure 3  
 XX  
 SQ Sequence 221 AA;

Query Match 100.0%; Score 943; DB 2; Length 221;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-92;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQQTAAALQKELKRIKIPDYS 60  
 DB 10 CNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQQTAAALQKELKRIKIPDYS 69  
 QY 61 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMPVNVGLKFSISNANIKISGKWKAKQKRF 120  
 DB 70 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMPVNVGLKFSISNANIKISGKWKAKQKRF 129  
 QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKSKVGLIQLF 180  
 DB 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKSKVGLIQLF 189  
 QY 181 HKKI 184  
 DB 190 HKKI 193

RESULT 3  
 ID AAW16800 standard; protein; 230 AA.  
 XX AAW16800;  
 XX 28-JUL-1997 (first entry)  
 DT Recombinant endotoxin neutralising polypeptide NCY108.  
 DE  
 XX Recombinant; endotoxin; neutralisation; RNP; NCY108; lipopolysaccharide;  
 KW LPS; bactericidal; permeability; increase; BPI; detection; Gram-negative;  
 KW bacterium; infection; prevention; treatment; disorder; mediation;  
 KW stimulation; neutrophil; mononuclear cell; inhibition; shock; anemia;  
 KW anaemia; disseminated intravascular coagulation; thrombocytopenia;  
 KW thrombocytopenia; adult respiratory distress syndrome; ARDS;  
 KW renal failure; liver disease; half life; human.  
 XX Homo sapiens.  
 OS Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 PH Peptide 1. .31  
 FT /label= sig\_peptide  
 FT  
 PN WO9634873-A1.  
 XX

PD 07-NOV-1996.  
 XX  
 XX  
 PF 01-MAY-1996; 96WO-US006134.  
 XX  
 XX  
 PR 01-MAY-1995; 95US-00431517.  
 XX  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 XX  
 PI Scott RW, Marra MN;  
 XX  
 XX  
 DR WPI; 1996-506090/50.  
 XX  
 XX  
 PT Lipo:polysaccharide binding and endotoxin neutralising polypeptide -  
 XX useful in diagnosis, prevention and treatment of Gram-negative bacterial  
 XX infection and associated disorders and conditions.  
 XX  
 XX  
 PS Example 1; Page; 147pp; English.  
 XX  
 XX  
 CC The present sequence is the recombinant endotoxin neutralising  
 CC polypeptide (RENPE) B(1-199) (NCY108), which comprises residues 1-199 of  
 CC human bactericidal/permeability increasing protein (hBPI). The RENPE,  
 CC which selectively and specifically binds lipopolysaccharide (LPS) and has  
 CC endotoxin neutralising activity, can be used to detect a site of Gram  
 CC negative bacterial infection, and prevent or treat endotoxin related  
 CC disorders, preferably where LPS mediated stimulation of neutrophils and  
 CC mononuclear cells is inhibited, e.g. shock, disseminated intravascular  
 CC coagulation, anaemia, thrombocytopenia, adult respiratory distress  
 CC syndrome, renal failure, liver disease and conditions associated with  
 CC Gram negative bacterial infection. The RENPE has an enhanced serum half  
 CC life relative to naturally occurring BPI, and binds LPS without  
 CC triggering a significant, undesirable immune response. N.B. Sequence not  
 CC given in specification, but produced using the wild type hBPI sequence  
 XX given in figure 3  
 XX  
 SQ Sequence 230 AA;  
 Query Match 100.0%; Score 943; DB 2; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-92;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRSQKGLDYASQOQTAAALQKELKRIKIPDYS 60  
 DB 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVRSQKGLDYASQOQTAAALQKELKRIKIPDYS 69  
 QY 61 DSFKIKHLGKGHYFSYMDIREFQLPSSQISWPNVNLKFSISNANIKISGKWKAKQKRF 120  
 DB 70 DSFKIKHLGKGHYFSYMDIREFQLPSSQISWPNVNLKFSISNANIKISGKWKAKQKRF 129  
 QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKVGVWLIQLF 180  
 DB 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKVGVWLIQLF 189  
 QY 181 HKKI 184  
 DB 190 HKKI 193  
 RESULT 4  
 AAW47091  
 ID AAW47091 standard; protein; 230 AA.  
 XX  
 AC AAW47091;  
 XX  
 DT 18-MAY-1998 (first entry)  
 XX  
 DE Human recombinant BPI (rBPI23) protein.  
 XX  
 KW Bactericidal/permeability increasing protein; BPI; clot formation; TA;  
 KW clot dissolution; thrombosis; thrombolytic agent; recombinant.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.

FH Key Location/Qualifiers  
 FT Peptide 1..31  
 FT /note= "signal sequence"  
 FT Protein 32..230  
 FT /note= "mature recombinant rBPI23 protein"  
 FT Misc-difference 216  
 FT /label= K216E  
 FT /note= "wild-type Lys is replaced by Glu"  
 FN WO9742967-A1.  
 XX  
 XX  
 PD 20-NOV-1997.  
 XX  
 XX  
 PF 09-MAY-1997; 97WO-US008017.  
 XX  
 XX  
 PR 10-MAY-1996; 96US-00644290.  
 XX  
 XX (XOMA ) XOMA CORP.  
 XX  
 XX White ML, Ammons WS;  
 XX  
 XX WPI; 1998-008579/01.  
 XX  
 XX N-PSDB; AAV13962.  
 XX  
 XX Use of bactericidal/permeability-increasing protein products - for  
 XX slowing clot formation and enhancing clot dissolution in blood,  
 XX particularly for treating thrombotic disorders.  
 XX  
 XX Example 1; Page; 56pp; English.  
 XX  
 XX This is a recombinant bactericidal/permeability-increasing (BPI) protein  
 XX product rBPI23. A BPI protein product can be administered especially by  
 XX contacting with blood to delay or prevent clot formation in the blood or  
 XX to enhance clot dissolution in the blood. A BPI protein product can also  
 XX be administered, optionally with a thrombolytic agent (TA), to treat a  
 XX patient suffering from thrombotic disorders such as arterial thrombosis,  
 XX coronary artery thrombosis, myocardial infarction, cerebral artery  
 XX thrombosis, stroke, intracardiac thrombosis, peripheral arterial  
 XX thrombosis or occlusion, venous thrombosis, pulmonary embolism,  
 XX thrombosis associated with exposure of blood to a foreign or injured  
 XX tissue surface, hypercoagulability, non-endotoxin-associated  
 XX coagulopathies, and non-endotoxin-associated disseminated intravascular  
 XX coagulopathy. The BPI protein products can be used in a method for  
 XX enhancing reperfusion or reducing reocclusion in a subject treated with a  
 XX TA comprising co-administration of the BPI protein product and the TA and  
 XX in a method for decreasing the dose of a TA required to establish  
 XX reperfusion or to reduce reocclusion in a subject comprising co-  
 XX administration of a BPI protein product and a TA, the dosage of the TA  
 XX being less than that required for a desired pharmaceutical effect when  
 XX the TA is administered as a monotherapy. The BPI protein products have  
 XX anticoagulant and thrombolytic activity and can be used for the  
 XX prophylactic and therapeutic treatment of thrombotic disorders. The BPI  
 XX products can be used to reduce the dosage of antithrombotic agent  
 XX required, thereby reducing or eliminating potential side effects. Note:  
 XX This sequence is not provided in the specification. It has been created  
 XX by modifying the natural BPI protein sequence given in Pages 46-48 of the  
 XX specification  
 XX  
 SQ Sequence 230 AA;  
 Query Match 100.0%; Score 943; DB 2; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-92;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRSQKGLDYASQOQTAAALQKELKRIKIPDYS 60  
 DB 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVRSQKGLDYASQOQTAAALQKELKRIKIPDYS 69  
 QY 61 DSFKIKHLGKGHYFSYMDIREFQLPSSQISWPNVNLKFSISNANIKISGKWKAKQKRF 120  
 DB 70 DSFKIKHLGKGHYFSYMDIREFQLPSSQISWPNVNLKFSISNANIKISGKWKAKQKRF 129  
 QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKVGVWLIQLF 180

```
|||||
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKSKVGLIQLF 189
Qy 181 HKKI 184
Db 190 HKKI 193

RESULT 5
AAR33777
AC AAR33777 standard; protein; 243 AA.
XX
XX
XX 25-MAR-2003 (revised)
DT 22-JUL-1993 (first entry)
XX
XX BPIP from p212.
XX
XX Bacterial/permeability increasing protein; lipopolysaccharide; LPS;
KW inhibitor; endotoxin-related shock;
KW disseminated intravascular coagulation; anaemia; thrombocytopenia; ARDS;
KW renal failure; endotoxaemia; adult respiratory distress syndrome.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..32 "signal peptide"
FT Region 32..243
FT /note= "mature protein"
XX
XX WO9305797-A1.
XX
XX 01-APR-1993.
XX
XX 28-SEP-1992; 92WO-US008234.
XX
XX 27-SEP-1991; 91US-00766566.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Marra MN, Scott RW, Snable JL, Wilde CG;
XX WPI; 1993-117241/14.
XX
XX Compens. contg. a bactericidal and permeability increasing protein -
XX solubilised in a lipid carrier to maintain stably an active form.
XX
XX Disclosure; Fig 7; 53pp; English.
XX
XX The human bactericidal/permeability increasing protein may be used in a
XX compsn. solubilised in a lipid carrier. The BPIP binds
XX lipopolysaccharides and inhibits the immunostimulatory and toxic
XX activities of LPS in vitro and in vivo. The lipid compsn. stably
XX maintains the BPIP in a sol. active form. The compsn. can be used for
XX detecting or quantifying LPS in a sample, coating a surgical tool.
XX coating an implantable invasive device, decontaminating a fluid contg.
XX LPC and treating endotoxin related -shock, -disseminated intravascular
XX coagulation, -anaemia, -thrombocytopenia, -adult respiratory stress
XX syndrome or -renal failure, or for preventing endotoxaemia. See also
XX AAR33776, AAR33729-31. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 243 AA;
XX
XX Query Match 100.0%; Score 943; DB 2; Length 243;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-92;
XX Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 CNAPRWLSMLVLAIGTAVTAANPGVVVRISQKGLDYASQQTAAALQKELKRIKIPDYS 60
Db 10 CNAPRWLSMLVLAIGTAVTAANPGVVVRISQKGLDYASQQTAAALQKELKRIKIPDYS 69
```

---

```
Qy 61 DSFKIKHLGKHGHSFYSDMIREQLPSSQISMVNVLKPSISNANIKISGKWAQKRFL 120
Db DSEFKIKHLGKHGHSFYSDMIREQLPSSQISMVNVLKPSISNANIKISGKWAQKRFL 129
Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKSKVGLIQLF 180
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKSKVGLIQLF 189
Qy 181 HKKI 184
Db 190 HKKI 193

RESULT 6
AAW16803
ID AAW16803 standard; protein; 243 AA.
XX
XX AAW16803;
XX
XX 28-JUL-1997 (first entry)
XX
XX Recombinant endotoxin neutralising polypeptide Lot #159693.
XX
XX Recombinant; endotoxin; neutralisation; RENP; Lot #159693;
KW lipopolysaccharide; LPS; bactericidal; permeability; increase; BPI;
KW detection; Gram-negative; bacterium; infection; prevention; treatment;
KW disorder; mediation; stimulation; neutrophil; mononuclear cell;
KW inhibition; shock; anaemia;
KW disseminated intravascular coagulation; thrombocytopenia;
KW thrombocytopenia; adult respiratory distress syndrome; ARDS;
KW renal failure; liver disease; half life; human.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Peptide 1..31
FT /label= sig_peptide
XX
XX WO9634873-A1.
XX
XX 07-NOV-1996.
XX
XX 01-MAY-1996; 96WO-US006134.
XX
XX 01-MAY-1995; 95US-00431517.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Scott RW, Marra MN;
XX WPI; 1996-506090/50.
XX
XX Lipo;polysaccharide binding and endotoxin neutralising polypeptide -
XX useful in diagnosis, prevention and treatment of Gram-negative bacterial
XX infection and associated disorders and conditions.
XX
XX Example 1; Page; 147pp; English.
XX
XX The present sequence is the recombinant endotoxin neutralising
XX polypeptide (RENP) B(1-212) (Lot #159693), which comprises residues 1-212
XX of human bactericidal/permeability increasing protein (hBPI). The RENP,
XX which selectively and specifically binds lipopolysaccharide (LPS) and has
XX endotoxin neutralising activity, can be used to detect a site of Gram
XX negative bacterial infection, and prevent or treat endotoxin related
XX disorders, preferably where LPS mediated stimulation of neutrophils and
XX mononuclear cells is inhibited, e.g. shock, disseminated intravascular
XX coagulation, anaemia, thrombocytopenia, adult respiratory distress
XX syndrome, renal failure, liver disease and conditions associated with
XX Gram negative bacterial infection. The RENP has an enhanced serum half
XX life relative to naturally occurring BPI, and binds LPS without
XX triggering a significant, undesirable immune response. N.B. Sequence not
XX given in specification, but produced using the wild type hBPI sequence
```

```
CC given in figure 3
XX Sequence 243 AA;
SQ
    Query Match      100.0%; Score 943; DB 2; Length 243;
    Best Local Similarity 100.0%; Pred. No. 1.8e-92;
    Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAAVNPVGVRISQKGLDYASQGGTAALQKELKRIKIPDYS 60
Db 10 CNAPRWVSLMVLVAIGTAVTAAVNPVGVRISQKGLDYASQGGTAALQKELKRIKIPDYS 69
Qy 61 DSFKIKHLGKHGHSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISGKWAQKRF 120
Db 70 DSFKIKHLGKHGHSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISGKWAQKRF 129
Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHISKVGLWLIQLF 180
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHISKVGLWLIQLF 189
Qy 181 HKKI 184
Db 190 HKKI 193

RESULT 7
AAW16802
ID AAW16802 standard; protein; 267 AA.
XX
AC AAW16802;
XX
DT 28-JUL-1997 (first entry)
XX
DE Recombinant endotoxin neutralising polypeptide Lot #159695.
XX
KW Recombinant; endotoxin; neutralisation; RNP; Lot #159695;
KW lipopolysaccharide; LPS; bactericidal; permeability; increase; BPI;
KW detection; Gram-negative; bacterium; infection; prevention; treatment;
KW disorder; mediation; stimulation; neutrophil; mononuclear cell;
KW inhibition; shock; anaemia; anaemia;
KW disseminated intravascular coagulation; thrombocytopenia;
KW thrombocytopenia; adult respiratory distress syndrome; ARDS;
KW renal failure; liver disease; half life; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..31
FT /label= sig_peptide
XX
PN WO9634873-A1.
XX
PD 07-NOV-1996.
XX
PF 01-MAY-1996; 96WO-US006134.
XX
PR 01-MAY-1995; 95US-00431517.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Scott RW, Marra MN;
XX
DR WPI; 1996-506090/50.
XX
PT Lipo:polysaccharide binding and endotoxin neutralising polypeptide -
PT useful in diagnosis, prevention and treatment of Gram-negative bacterial
PT infection and associated disorders and conditions.
XX
XX Example 1; Page; 147pp; English.
XX
PS The present sequence is the recombinant endotoxin neutralising
CC polypeptide (RNP) B(1-236) (Lot #159695), which comprises residues 1-236
```

```
CC of human bactericidal/permeability increasing protein (hBPI). The RNP,
CC which selectively and specifically binds lipopolysaccharide (LPS) and has
CC endotoxin neutralising activity, can be used to detect a site of Gram
CC negative bacterial infection, and prevent or treat endotoxin related
CC disorders, preferably where LPS mediated stimulation of neutrophils and
CC mononuclear cells is inhibited, e.g. shock, disseminated intravascular
CC coagulation, anaemia, thrombocytopenia, adult respiratory distress
CC syndrome, renal failure, liver disease and conditions associated with
CC Gram negative bacterial infection. The RNP has an enhanced serum half
CC life relative to naturally occurring BPI, and binds LPS without
CC triggering a significant, undesirable immune response. N.B. Sequence not
CC given in specification, but produced using the wild type hBPI sequence
CC given in figure 3
XX
SQ Sequence 267 AA;
    Query Match      100.0%; Score 943; DB 2; Length 267;
    Best Local Similarity 100.0%; Pred. No. 1.8e-92;
    Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAAVNPVGVRISQKGLDYASQGGTAALQKELKRIKIPDYS 60
Db 10 CNAPRWVSLMVLVAIGTAVTAAVNPVGVRISQKGLDYASQGGTAALQKELKRIKIPDYS 69
Qy 61 DSFKIKHLGKHGHSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISGKWAQKRF 120
Db 70 DSFKIKHLGKHGHSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISGKWAQKRF 129
Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHISKVGLWLIQLF 180
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHISKVGLWLIQLF 189
Qy 181 HKKI 184
Db 190 HKKI 193

RESULT 8
AAW62410
ID AAW62410 standard; protein; 300 AA.
XX
AC AAW62410;
XX
DT 01-OCT-1998 (first entry)
XX
DE Bactericidal permeability increasing factor #1.
XX
KW Bactericidal; Pseudomonas sp; endotoxin shock; bacterial infection;
KW bactericidal permeability increasing factor; B/Pi; neutralising;
KW human neutrophil granule bactericidal protein.
XX
OS Homo sapiens.
XX
PN US5786324-A.
XX
PD 28-JUL-1998.
XX
PF 24-MAR-1994; 94US-00218026.
XX
PR 24-MAR-1994; 94US-00218026.
XX
PA (MINU) UNIV MINNESOTA.
XX
PI Mayo K, Haseman JR, Gray B;
XX
DR WPI; 1998-436578/37.
XX
DR N-PSDB; AAY39860.
XX
PT Bactericidal and endotoxin-neutralising peptides - used in treating e.g.
PT Pseudomonas species infection and in protectively coating prosthetic
PT devices.
XX
PS Example 1; Fig 4; 46pp; English.
```

XX The present invention describes bactericidal peptides (BP): (a) for  
 CC Pseudomonas species; (b) with endotoxin neutralising activity; (c) with  
 CC both endotoxin neutralising activity and bactericidal activity; for  
 CC Pseudomonas aeruginosa; (d) a hybrid peptide with endotoxin neutralising  
 CC activity and bactericidal activity, the peptide having at least 1 amino  
 CC acid sequence of a peptide with endotoxin neutralising activity combined  
 CC with at least 1 different amino acid sequence of a peptide that has  
 CC bactericidal activity; and (e) a prosthetic device which has a sufficient  
 CC amount of BP attached to the surface to inhibit bacterial growth. The  
 CC peptides of the invention are used in treating bacterial infection such  
 CC as Pseudomonas strains e.g. for P. aeruginosa at 10<sup>-7</sup> to 10<sup>-9</sup> M, and  
 CC Escherichia coli. The peptides are also used to treat endotoxin shock.  
 CC The present sequence represents bactericidal permeability increasing  
 CC factor from an example of the present invention

XX  
 SQ Sequence 300 AA;

Query Match 100.0%; Score 943; DB 2; Length 300;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAANNPGVVVRISQKGLDYASQQTAAALQKELKIKIPDYS 60  
 |||||  
 Db 10 CNAPRWVSLMVLVAIGTAVTAANNPGVVVRISQKGLDYASQQTAAALQKELKIKIPDYS 69  
 |||||

Qy 61 DSFKIKHLGKHGHSFYSDIREFQLPSSQISMPVNVGLKFSISNANIKISGKWKAKRFL 120  
 |||||  
 Db 70 DSFKIKHLGKHGHSFYSDIREFQLPSSQISMPVNVGLKFSISNANIKISGKWKAKRFL 129  
 |||||

Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTTCSSCSHINSVHVHISKSKVGMWLIQLF 180  
 |||||  
 Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTTCSSCSHINSVHVHISKSKVGMWLIQLF 189  
 |||||

Qy 181 HKKI 184  
 |||||  
 Db 190 HKKI 193

RESULT 9  
 AAR21840  
 ID AAR21840 standard; protein; 368 AA.

XX  
 AC AAR21840;

XX 22-JUL-1992 (first entry)

XX Human 57kd protein p337 which binds to the outer membrane of susceptible  
 DE gram negative bacteria (BPI).

XX Endotoxin binding protein; diagnosis; therapy; endotoxemia;  
 KW endotoxic shock.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FT Region 1..31  
 FT /label= residues -31 to -1

XX WO9203535-A.

XX 05-MAR-1992.

XX 13-AUG-1991; 91WO-US005758.

XX 13-AUG-1990; 90US-00567016.

XX 05-APR-1991; 91US-00681551.

XX (INCY-) INCYTE PHARM INC.

XX Marra MN, Scott RW;

XX WPI; 1992-096879/12.

XX New recombinant BPI protein - specifically binds to and inhibits  
 PT endotoxin lethality, for prevention, treatment and diagnosis of endo-  
 PT toxemia and endo-toxic shock.

XX Disclosure; Fig 13; 108pp; English.

XX The BPI binds endotoxin in the presence of serum and plasma and, unlike  
 CC other known endotoxin binding proteins such as LBP (lipopolysaccharide  
 CC binding protein), BPI inhibits the immunostimulatory and toxic activities  
 CC of endotoxin both in vitro and in vivo. Thus BPI can be used in the  
 CC diagnosis and therapeutic and prophylactic treatment of endotoxin-related  
 CC disorders including endotoxemia and endotoxic shock

XX Sequence 368 AA;

Query Match 100.0%; Score 943; DB 2; Length 368;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-92;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAANNPGVVVRISQKGLDYASQQTAAALQKELKIKIPDYS 60  
 |||||

Db 10 CNAPRWVSLMVLVAIGTAVTAANNPGVVVRISQKGLDYASQQTAAALQKELKIKIPDYS 69  
 |||||

Qy 61 DSFKIKHLGKHGHSFYSDIREFQLPSSQISMPVNVGLKFSISNANIKISGKWKAKRFL 120  
 |||||

Db 70 DSFKIKHLGKHGHSFYSDIREFQLPSSQISMPVNVGLKFSISNANIKISGKWKAKRFL 129  
 |||||

Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTTCSSCSHINSVHVHISKSKVGMWLIQLF 180  
 |||||

Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTTCSSCSHINSVHVHISKSKVGMWLIQLF 189  
 |||||

Qy 181 HKKI 184  
 |||||

Db 190 HKKI 193

RESULT 10

AAR71291

ID AAR71291 standard; protein; 368 AA.

XX AC AAR71291;

XX 25-MAR-2003 (revised)

XX 02-SEP-1995 (first entry)

XX Human bactericidal-permeability increasing protein p337 variant.

XX Antibiotic; permeability increasing protein; p337 variant;  
 KW endotoxin binding protein.

XX Homo sapiens.

XX WO9501428-A1.

XX 12-JAN-1995.

XX 01-JUL-1994; 94WO-US007466.

XX 02-JUL-1993; 93US-00087484.

XX (INCY-) INCYTE PHARM INC.

XX Marra MN, Scott RW, Lane JC, Snable JL;

XX WPI; 1995-060992/08.

XX Non-glycosylated bactericidal-permeability increasing protein prodn. - by  
 PT culturing transformed Gram-negative bacteria, useful as antibacterial  
 PT agent.

XX Disclosure; Fig 9; 82pp; English.

CC p337 protein is a 38 kDa non-glycosylated variant of human bactericidal-  
CC permeability increasing protein (see AAR71290), which has antibacterial  
CC activity against Gram-negative bacteria, inhibits lipopolysaccharide  
CC (LPS) directly, and inhibits LPS- mediated tumor necrosis factor  
CC production from mononuclear cells. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
XX  
SQ Sequence 368 AA;  
Query Match 100.0%; Score 943; DB 2; Length 368;  
Best Local Similarity 100.0%; Pred. No. 2.8e-92; Mismatches 0; Indels 0; Gaps 0;  
Matches 184; Conservative 0;  
QY 1 CNAFRWVSLMVLVAIGTAVTAAVNPVGVVVRISQKGLDYASQGTAAALQKELKRIKIPDYS 60  
DB 10 CNAFRWVSLMVLVAIGTAVTAAVNPVGVVVRISQKGLDYASQGTAAALQKELKRIKIPDYS 69  
QY 61 DSFKIKHLGKGHYSPYSMDIREFQLPSSQISWVPNVGLKFSISNANIKISGKWKAKRFL 120  
DB 70 DSFKIKHLGKGHYSPYSMDIREFQLPSSQISWVPNVGLKFSISNANIKISGKWKAKRFL 129  
QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKSKVGLIQLF 180  
DB 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKSKVGLIQLF 189  
QY 181 HKKI 184  
DB 190 HKKI 193  
RESULT 11  
AAB66058  
ID AAB66058 standard; protein; 483 AA.  
XX  
AC AAB66058;  
XX  
XX 30-MAR-2001 (first entry)  
XX Human Bactericidal Permeability Increasing, BPI protein.  
XX  
XX Gene therapy; TANGO protein; INTERCEPT protein; neurological disorder;  
KW central nervous system; focal brain disorder; bipolar affective disorder;  
KW global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease;  
KW senile dementia; Huntington's disease; amyotrophic lateral sclerosis;  
KW Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep;  
KW neuropsychiatric; psychoactive substance use; anxiety.  
XX  
OS Homo sapiens.  
XX  
XX WO200077239-A2.  
XX  
XX 21-DEC-2000.  
XX  
XX 24-MAY-2000; 2000WO-US014859.  
XX  
XX 14-JUN-1999; 99US-00333159.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX McCarthy SA, Fraser CC, Sharp JD, Barnes TM;  
PI WPI; 2001-032313/04.  
XX  
XX TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for  
PT screening assays and diagnostic assays and for the treatment of  
PT neurological diseases such as Alzheimer's, Parkinson's and Huntington's  
PT disease.  
XX  
XX Claim 8; Fig 5; 359pp; English.  
XX  
XX The present invention relates to TANGO or INTERCEPT proteins and coding  
CC sequences (see AAF45121-F45136 and AAF45138-F45139 and AAB66031-B66057,  
CC AAB66064-B66083 and AAB66085). The TANGO/INTERCEPT proteins and coding

CC sequences are useful for the treatment of neurological disorders such as  
CC central nervous system (CNS) disorders, CNS-related disorders, focal  
CC brain disorders, global-diffuse cerebral disorders and other neurological  
CC and cerebrovascular disorders. The CNS disorders include Alzheimer's  
CC disease, senile dementia, Huntington's disease, amyotrophic lateral  
CC sclerosis, Parkinson's, Gilles de la Tourette's syndrome, autonomic  
CC function disorders such as hypertension and sleep disorders,  
CC neuropsychiatric disorders, psychoactive substance use disorders,  
CC anxiety, and bipolar affective disorder. The present sequence is a  
CC sequence used in a sequence homology alignment with the TANGO/INTERCEPT  
CC sequences of the present invention  
XX  
XX SQ Sequence 483 AA;  
Query Match 100.0%; Score 943; DB 4; Length 483;  
Best Local Similarity 100.0%; Pred. No. 4.1e-92;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CNAFRWVSLMVLVAIGTAVTAAVNPVGVVVRISQKGLDYASQGTAAALQKELKRIKIPDYS 60  
DB 6 CNAFRWVSLMVLVAIGTAVTAAVNPVGVVVRISQKGLDYASQGTAAALQKELKRIKIPDYS 65  
QY 61 DSFKIKHLGKGHYSPYSMDIREFQLPSSQISWVPNVGLKFSISNANIKISGKWKAKRFL 120  
DB 66 DSFKIKHLGKGHYSPYSMDIREFQLPSSQISWVPNVGLKFSISNANIKISGKWKAKRFL 125  
QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKSKVGLIQLF 180  
DB 126 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKSKVGLIQLF 185  
QY 181 HKKI 184  
DB 186 HKKI 189  
RESULT 12  
ABO32712  
ID ABO32712 standard; protein; 483 AA.  
XX  
XX ABO32712;  
XX  
XX 17-SEP-2003 (first entry)  
XX Secreted polypeptide-related protein #90.  
XX  
XX Human; TANGO; INTERCEPT; secreted polypeptide; immune disorder;  
KW hormonal disorder; proliferative disorder; cancer; thyroid disorder;  
KW diabetes; multiple sclerosis; lupus; neurological disorder; anaemia;  
KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;  
KW myocardial infarction; congestive heart disease; blood platelet disorder;  
KW thrombocytopenia; blood vessel; atherosclerosis; vasculitis.  
XX  
XX Homo sapiens.  
XX  
XX US2003022279-A1.  
XX  
XX 30-JAN-2003.  
XX  
XX 12-JAN-2001; 2001US-00759130.  
XX  
XX 14-JUN-1999; 99US-00333159.  
PR 29-JUN-1999; 99US-00342364.  
PR 10-SEP-1999; 99US-00393996.  
PR 19-OCT-1999; 99US-00420707.  
PR 07-JAN-2000; 2000US-00479249.  
PR 27-APR-2000; 2000US-00559497.  
PR 24-MAY-2000; 2000US-00578063.  
PR 16-JUN-2000; 2000US-00596194.  
PR 23-JUN-2000; 2000US-00602871.  
PR 30-JUN-2000; 2000US-00608452.  
XX  
XX (FRAS/) FRASER C C.  
PA (BARN/) BARNES T M.



```
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (WACK/) WACKAY C R.
PA (GOOD/) GOODEARL A D J.
XX
XX Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;
PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;
XX
XX WPI; 2003-456290/43.
XX
XX New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202,
PT TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or
PT treating disorders such as cancer, diabetes or atherosclerosis, and in
PT forensic biology.
XX
XX Claim 9; Fig 28F-28G; 482pp; English.
XX
XX The invention relates to secreted polypeptide-related proteins and
CC nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The
CC nucleic acids, proteins and antibodies specific to the proteins are
CC useful in screening assays, predictive medicine (e.g. diagnostic assays,
CC prognostic assays, monitoring clinical trials and pharmacogenetics) and
CC prophylactic and therapeutic methods. The sequences are used in
CC diagnosing, preventing or treating proliferative disorders (e.g.
CC cancers), hormonal disorders (e.g. diabetes or thyroid disorders), immune
CC disorders (e.g. multiple sclerosis or lupus), neurological disorders
CC (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular
CC disorders (e.g. myocardial infarction or congestive heart disease), blood
CC platelet disorders (e.g. thrombocytopenia or anaemia) and disorders
CC involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic
CC acids may also be used in chromosome mapping, tissue typing and forensic
CC biology, and as surrogate markers. This sequence represents a secreted
CC polypeptide-related protein of the invention. Note: The sequence data for
CC this patent was obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
XX Sequence 483 AA;
XX
XX Query Match 100.0%; Score 943; DB 6; Length 483;
XX Best Local Similarity 100.0%; Pred. NO. 4.1e-92;
XX Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 60
Db 6 CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 65
QY 61 DSFKIKHLGKHGHSFYSGMDIREFOLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFL 120
Db 66 DSPKIKHLGKHGHSFYSGMDIREFOLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFL 125
QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKSKVGLIQLF 180
Db 126 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKSKVGLIQLF 185
QY 181 HKKI 184
Db 186 HKKI 189
XX
XX RESULT 13
XX ABU04504
ID ABU04504 standard; protein; 483 AA.
XX
XX AC ABU04504;
XX
XX 29--JAN-2003 (first entry)
XX
XX Human expressed protein tag (EPT) #1170.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
PA
XX Chicx RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1170; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 483 AA;
XX
XX Query Match 100.0%; Score 943; DB 6; Length 483;
XX Best Local Similarity 100.0%; Pred. NO. 4.1e-92;
XX Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 60
Db 6 CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 65
QY 61 DSFKIKHLGKHGHSFYSGMDIREFOLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFL 120
Db 66 DSPKIKHLGKHGHSFYSGMDIREFOLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFL 125
QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKSKVGLIQLF 180
Db 126 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKSKVGLIQLF 185
QY 181 HKKI 184
Db 186 HKKI 189
XX
XX RESULT 13
XX ABU04504
ID ABU04504 standard; protein; 483 AA.
XX
XX AC ABU04504;
XX
XX 29--JAN-2003 (first entry)
XX
XX Human expressed protein tag (EPT) #1170.
XX
XX
```



Db 186 HKKI 189

RESULT 14  
ABU04575

ID ABU04575 standard; protein; 483 AA.

XX AC ABU04575;

XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #1241.

XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009671.

XX PR 28-MAR-2001; 2001US-0279495P.

XX PR 21-MAY-2001; 2001US-0292544P.

XX PR 08-AUG-2001; 2001US-0310801P.

XX PR 01-OCT-2001; 2001US-0326370P.

XX PR 04-DEC-2001; 2001US-0336780P.

XX PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCOS INC.

XX PI Chicx RM, Tomlinson AJ, Urban RG;

XX DR WPI; 2003-040607/03.

XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.

XX PS Example 2; SEQ ID NO 1241; 134pp; English.

XX CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 483 AA;

Query Match 100.0%; Score 943; DB 6; Length 483;  
Best Local Similarity 100.0%; Pred. No. 4,1e-92;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQQTAAALQKELKRIKIPDYS 60  
|||||

Db 6 CNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQQTAAALQKELKRIKIPDYS 65

QY 61 DSFKIKHLGKHGHSFYSDIREFOLPSSQISWPNVGLKPSISNANIKISGKWKAKRFL 120  
|||||

Db 66 DSFKIKHLGKHGHSFYSDIREFOLPSSQISWPNVGLKPSISNANIKISGKWKAKRFL 125  
|||||

QY 121 KMSGNFDSLIRGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKSKVGLIOLF 180  
|||||

Db 126 KMSGNFDSLIRGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKSKVGLIOLF 185  
|||||

QY 181 HKKI 184

Db 186 HKKI 189

RESULT 15  
ADQ10386

ID ADQ10386 standard; protein; 483 AA.

XX AC ADQ10386;

XX DT 09-SEP-2004 (first entry)

XX DE Human polypeptide #206.

XX KW Human; cancer; obesity; gastritis; diarrhoea; haemorrhoid; asthma;  
KW anaemia; graft-versus-host reaction; allergic reaction; cystic fibrosis;  
KW hypogonadism; cardiovascular disorder; arthritis; osteoarthritis;  
KW arteriosclerosis; hypertension; bacterial infection; psoriasis;  
KW diabetes mellitus; hepatitis; Alzheimer's disease; Huntington's disease;  
KW Parkinson's disease; AIDS; tuberculosis; viral infection; malaria;  
KW goiter; infertility; endometriosis; muscular disorder.

XX OS Homo sapiens.

XX PN US2004121396-A1.

XX PD 24-JUN-2004.

XX PF 19-DEC-2003; 2003US-00741790.

XX PR 14-JUN-1999; 99US-00333159.

XX PR 29-JUN-1999; 99US-00342364.

XX PR 10-SEP-1999; 99US-00393996.

XX PR 19-OCT-1999; 99US-00420707.

XX PR 07-JAN-2000; 2000US-00479249.

XX PR 27-APR-2000; 2000US-00559497.

XX PR 24-MAY-2000; 2000US-00578063.

XX PR 16-JUN-2000; 2000US-00596194.

XX PR 23-JUN-2000; 2000US-00602871.

XX PR 30-JUN-2000; 2000US-00608452.

XX PR 12-JAN-2001; 2001US-00759130.

XX (MILL-) MILLENNIUM PHARM INC.

XX PA Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;  
PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;  
XX WPI; 2004-479675/45.

XX DR New TANGO, INTERCEPT, and MANGO, useful in diagnosing, preventing, and  
XX treating cancer, constipation, hemorrhoids, cystic fibrosis,  
PT hypogonadism, psoriasis, hepatitis, Alzheimer's disease, AIDS,  
PT tuberculosis, malaria, goiter, infertility.

XX PS Claim 9; SEQ ID NO 408; 483pp; English.

XX CC The invention relates to human polynucleotides and the polypeptides they  
CC encode. The invention also relates to a host cell containing a  
CC polynucleotide of the invention, an antibody which selectively binds with  
CC a polypeptide of the invention, a method of detecting the presence of a  
CC polypeptide in a sample, a method of identifying a compound which binds  
CC with a polypeptide, and a method of modulating the activity of a

CC polypeptide. The polynucleotides, polypeptides and compositions are  
CC useful for diagnosing, preventing and/or treating cancer, obesity, host  
CC gastritis, diarrhoea, haemorrhoids, asthma, anaemia, graft-versus-host  
CC reactions, allergic reactions, cystic fibrosis, hypogonadism,  
CC cardiovascular disorders, arthritis, osteoarthritis, arteriosclerosis,  
CC hypertension, bacterial infections, psoriasis, diabetes mellitus,  
CC hepatitis, Alzheimer's disease, Huntington's disease, Parkinson's  
CC disease, AIDS, tuberculosis, viral infections, malaria, goiter,  
CC infertility, endometriosis, wounds and muscular disorders. This sequence  
CC represents a human polypeptide of the invention. Note: The sequence data  
CC for this patent did not form part of the printed specification but was  
CC obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html.  
XX  
SQ

SQ Sequence 483 AA;  
Query Match 100.0%; Score 943; DB 8; Length 483;  
Best Local Similarity 100.0%; Pred. NO. 4,1e-92;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CNAPRWVSLMVLVAIGTAVTAAVNPVGWVVRISQKGLDYASQOQTAAQKELKIKIPDYS 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
6 CNAPRWVSLMVLVAIGTAVTAAVNPVGWVVRISQKGLDYASQOQTAAQKELKIKIPDYS 65  
Qy 61 DSPKIKHLGKGHYSFYSMDIREFQPSQISMPNVLKFSISNANIKSGKWKAKQKFL 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
66 DSPKIKHLGKGHYSFYSMDIREFQPSQISMPNVLKFSISNANIKSGKWKAKQKFL 125  
Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKXKVGWLIQLF 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
126 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKXKVGWLIQLF 185  
Qy 181 HKKI 184  
Db ||||  
186 HKKI 189

Search completed: October 21, 2005, 11:26:47  
Job time : 65.4411 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM\*protein - protein search, using sw model

Run on: October 21, 2005, 11:22:43 ; Search time 37.7407 Seconds  
(without alignments)  
1241.566 Million cell updates/sec

Title: US-10-629-516-2  
Perfect score: 2507  
Sequence: 1 MRENARGPCNAPRWVSLMV.....NVVLQPHQNFLLFGADVVK 487

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2507	100.0	487	A30909	bactericidal/permeability-increasing protein precursor - human
2	1627.5	64.9	482	S10180	bactericidal/permeability-increasing protein precursor - human
3	1288	51.4	250	S43383	bactericidal/permeability-increasing protein precursor - human
4	1087	43.4	481	A54136	lipopolysaccharide
5	1052	42.0	477	A35843	lipopolysaccharide
6	1039	41.4	481	I56246	lipopolysaccharide
7	985.5	39.3	482	B35843	lipopolysaccharide
8	465	18.5	493	A53533	phospholipid transfer protein
9	463.5	18.5	493	I42370	plasma phospholipid transfer protein
10	337.5	13.5	488	C86183	cholesterol transfer protein
11	295	11.8	493	A26941	cholesterol transfer protein
12	282	11.2	493	A53176	cholesterol transfer protein
13	271.5	10.8	497	I46692	cholesterol transfer protein
14	261.5	10.4	470	S17447	cholesterol transfer protein
15	234.5	9.4	473	S17448	cholesterol transfer protein
16	222	8.9	606	T29190	cholesterol transfer protein
17	205.5	8.2	487	T18952	cholesterol transfer protein
18	189	7.5	464	T16889	cholesterol transfer protein
19	186.5	7.4	486	T20482	cholesterol transfer protein
20	175	7.0	554	T15438	cholesterol transfer protein
21	174	6.9	576	T22700	cholesterol transfer protein
22	154	6.1	824	E87856	cholesterol transfer protein
23	154	6.1	846	T20710	cholesterol transfer protein
24	138	5.5	284	T29001	cholesterol transfer protein
25	122.5	4.9	412	T30079	cholesterol transfer protein
26	122	4.9	1134	T04587	cholesterol transfer protein
27	110	4.4	1234	B36186	cholesterol transfer protein
28	109	4.3	779	JH0102	cholesterol transfer protein
29	108	4.3	177	T29000	cholesterol transfer protein

30	105	4.2	733	2	A97415	hypothetical protein
31	104.5	4.2	980	2	H94632	probable receptor-cholesterol transfer protein
32	104	4.1	289	2	A38700	receptor protein kinase
33	104	4.1	981	2	T50851	bud emergence protein
34	104	4.1	1128	2	A49960	genome polyprotein
35	104	4.1	3005	1	GNVSTV	glycyl-tRNA synthetase
36	103	4.1	693	2	C83821	probable disease resistance protein
37	103	4.1	994	2	H96510	hypothetical protein
38	102.5	4.1	2218	2	B46883	probable peptide signal
39	101.5	4.0	4924	2	T50176	translation initiation factor
40	101	4.0	831	2	H97801	apolipoprotein B-100
41	100.5	4.0	784	2	JH0101	D-alanine aminotransferase
42	100	4.0	499	2	E86782	carbamoyl transfer protein
43	100	4.0	534	2	G75093	conserved hypothetical protein
44	100	4.0	956	2	H81654	hypothetical protein
45	100	4.0	4307	2	T20721	hypothetical protein

ALIGNMENTS

RESULT 1

A30909  
N:Alterate names: SSK bactericidal protein  
C:Species: Homo sapiens (man)  
C:Date: 18-Apr-1989 #sequence revision 18-Apr-1989 #text change 09-Jul-2004  
C:Accession: A33850; B54136; A29464; A43600; A49716; A30909  
R:Gray, P.W.; Flagg, G.; Leong, S.R.; Gumina, R.J.; Weiss, J.; Ooi, C.E.; Elsbach, P.  
J. Biol. Chem. 264, 9505-9509, 1989  
A:Title: Cloning of the cDNA of a human neutrophil bactericidal protein. Structural and  
A:Reference number: A33850; MUID:89255455; PMID:2722846  
A:Accession: A33850  
A:Molecule type: mRNA  
A:Residues: 1-487 <GRA>  
A:Cross-references: UNIPROT:Q9UCT4; GB:J04739; NID:q179528; PID:AAAS1841.1; PID:gi79529  
R:Wilde, C.G.; Seilhamer, J.J.; McGrogan, M.; Ashton, N.; Snable, J.B.; Lane, J.C.; Leon  
J. Biol. Chem. 269, 17411-17416, 1994  
A:Title: Bactericidal/permeability-increasing protein and lipopolysaccharide (LPS)-binding  
A:Reference number: A54136; MUID:94292492; PMID:7517398  
A:Accession: B54136  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-374, 'L', 376-487 <WIL>  
A:Experimental source: HL-60 cells  
A:Note: sequence extracted from NCBI backbone (NCBI:149855)  
R:Ooi, C.E.; Weiss, J.; Elsbach, P.; Frangione, B.; Mannion, B.  
J. Biol. Chem. 262, 14891-14894, 1987  
A:Title: A 25-Kda amino-terminal fragment carries all the antibacterial activities of the  
A:Reference number: A29464; MUID:88033057; PMID:3667613  
A:Accession: A29464  
A:Molecule type: protein  
A:Residues: 32-51 <OOI>  
A:Experimental source: neutrophils  
R:Wasiluk, K.R.; Skubitz, K.M.; Gray, B.H.  
Infect. Immun. 59, 4193-4200, 1991  
A:Title: Comparison of granule proteins from human polymorphonuclear leukocytes which ar  
A:Reference number: A43600; MUID:92040097; PMID:1937776  
A:Accession: A43600  
A:Molecule type: protein  
A:Residues: 32-52, 'R' <WAS>  
R:Little, R.G.; Kainer, D.N.; Lim, E.; Burke, D.J.; Conlon, P.J.  
J. Biol. Chem. 269, 1865-1872, 1994  
A:Title: Functional domains of recombinant bactericidal/permeability-increasing protein  
A:Reference number: A49716; MUID:94124531; PMID:8294435  
A:Accession: A49716  
A:Molecule type: protein  
A:Residues: 32-130, 132-141, 143-165, 202-215, 'E', 217-225 <LIT>  
C:Comment: The bactericidal/permeability-increasing protein (BPI) is a 60 kD membrane-as  
which is specific for gram-negative bacteria. BPI has a high affinity for lipopolysacchar  
between BPI and an LPS-binding protein from liver and cholesterol ester transfer protein  
C:Genetics:  
A:Gene: GDB:BPI

A;Cross-references: GDB:131572; OMIM:109195  
A;Map position: 20q11.23-20q12  
C;Superfamily: lipopolysaccharide-binding protein  
C;Keywords: antibacterial; cytotoxin; glycoprotein; heparin binding; neutrophil  
F;1-31/Domain: signal sequence #status predicted <SIG>  
F;32-487/Product: bactericidal permeability-increasing protein #status predicted <MAT>  
F;32-51/Region: bactericidal #status predicted  
F;380/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 2507; DB 2; Length 487;  
Best Local Similarity 100.0%; Pred. No. 1.4e-186;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENWARGPCNAPRWVSLMWLVVAIGTAVTAANPGVVVRIISQKGLDYASQGTAAALQKEL 60  
Db 1 MRENWARGPCNAPRWVSLMWLVVAIGTAVTAANPGVVVRIISQKGLDYASQGTAAALQKEL 60  
Qy 61 KRKIPDYSDFKIKHLGKHGHSFYSDIREFOLPSSQISWPNVGLKFSISNANIKISG 120  
Db 61 KRKIPDYSDFKIKHLGKHGHSFYSDIREFOLPSSQISWPNVGLKFSISNANIKISG 120  
Qy 121 KWAQKRFKLVKSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKS 180  
Db 121 KWAQKRFKLVKSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKS 180  
Qy 181 KVGHLLIQLFHKKTESALRNKNSQVCEKVTNSVSKLQPYFQTLPVMTKIDSVAGINYL 240  
Db 181 KVGHLLIQLFHKKTESALRNKNSQVCEKVTNSVSKLQPYFQTLPVMTKIDSVAGINYL 240  
Qy 241 VAPPATTAETLDVQMKGEFYSNHNPPPPAPPVMEFPAADHVMVGLGLSDYFNTAGLV 300  
Db 241 VAPPATTAETLDVQMKGEFYSNHNPPPPAPPVMEFPAADHVMVGLGLSDYFNTAGLV 300  
Qy 301 YQKAGVLKMTLRDDMI PKESKFRLLTKFFGTFLEPAVKFPNMKI QIHVSASTPPHLSVQ 360  
Db 301 YQKAGVLKMTLRDDMI PKESKFRLLTKFFGTFLEPAVKFPNMKI QIHVSASTPPHLSVQ 360  
Qy 361 PTGLTTFPAVDVQAFVLPNSSLASLFLIGHHTTGSMEVSAESNRLVGEKLDRLLEL 420  
Db 361 PTGLTTFPAVDVQAFVLPNSSLASLFLIGHHTTGSMEVSAESNRLVGEKLDRLLEL 420  
Qy 421 HSNIGPFPVELLDIMNYIPIVLPRVNEKLOKGFPLTPARVOLNVVLPQHONFLLF 480  
Db 421 HSNIGPFPVELLDIMNYIPIVLPRVNEKLOKGFPLTPARVOLNVVLPQHONFLLF 480  
Qy 481 GADVYVK 487  
Db 481 GADVYVK 487

RESULT 2  
S10180  
bactericidal permeability-increasing protein precursor - bovine  
C;Species: Bos primigenius taurus (Cattle)  
C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004  
C;Accession: S10180  
R;Leong, S.R.; Camerato, T.  
Nucleic Acids Res. 18, 3052, 1990  
A;Title: Nucleotide sequence of the bovine bactericidal permeability increasing protein  
A;Reference number: S10180; MUID:90272418; PMID:2349103  
A;Accession: S10180  
A;Molecule type: mRNA  
A;Residues: 1-482 <LSO>  
A;Cross-references: UNIPROT:P17453; EMBL:X52563; NID:gl38; PIDN:CAA36797.1; PID:gl39  
C;Superfamily: lipopolysaccharide-binding protein  
F;1-26/Domain: signal sequence #status predicted <SIG>  
F;27-482/Product: bactericidal permeability increasing protein #status predicted <MAT>

Query Match 64.9%; Score 1627.5; DB 2; Length 482;  
Best Local Similarity 63.5%; Pred. No. 2.5e-118;  
Matches 306; Conservative 81; Mismatches 94; Indels 1; Gaps 1;

Qy 5 MARGPCNAPRWVSLMWLVVAIGTAVTAANPGVVVRIISQKGLDYASQGTAAALQKELKRIK 64

Db 1 MARGPDTARRWATLVVLAALGTAVT-TTNPGLVARITQKGLDYACQGVLTQKLEKIT 59  
Qy 65 IPDYSDFKIKHLGKHGHSFYSDIREFOLPSSQISWPNVGLKFSISNANIKISGKWA 124  
Db 60 IPNFSNFKIKYLGKQYSSFFSVIQQFNLPNSQIRPLDKGLDLSIRASIKIRGKWA 119  
Qy 125 OKRFLKWSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSVGW 184  
Db 120 RKNFIKLGNGFDLSVSGISILAGNLGYPASGHSVTTCSSCSGINTVRIHISGSLGW 179  
Qy 185 LIQLFHKKIESALRNKNSQVCEKVTNSVSKLQPYFQTLPVMTKIDSVAGINYLVA 244  
Db 180 LIQLFKRIEISLLQKSWTRKICEVVTSTVSSKLOPYFQTLPTVTKLDKAGVDYSLVAPP 239  
Qy 245 ATTAETLDVQMKGEFYSNHNPPPPAPPVMEFPAADHVMVGLGLSDYFNTAGLVQEA 304  
Db 240 RATANNLLMLLKGFEFFSLAHRSPPPAPPALAPFSDHDMVYLGISSEYFNTAGVYQKA 299  
Qy 305 GVLKMTLRDDMI PKESKFRLLTKFFGTFLEPAVKFPNMKI QIHVSASTPPHLSVQPTGL 364  
Db 300 GANLTLRDDMI PKESKFRLLTKFFGILIPQVAKMFPDMQQLFIWASLPPLTKMFPSSL 359  
Qy 365 TFYPADVQAFVLPNSSLASLFLIGHHTTGSMEVSAESNRLVGEKLDRLLELKHNI 424  
Db 360 DLIFVLDTOAFVLPNSSLDPLFLEMLNLSVVVGAKSDRLIGELRLDKLLELKHSDI 419  
Qy 425 GPPVELLDIMNYIPIVLPRVNEKLOKGFPLTPARVOLNVVLPQHONFLFGADV 484  
Db 420 GPFVSLSQSVINVMPTVLPVINKLOKGFPLPAYIEFLNLTLPQYQDFLLFGADV 479  
Qy 485 VY 486  
Db 480 QY 481

RESULT 3  
S43383  
bactericidal/permeability-increasing protein - synthetic  
C;Species: synthetic  
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C;Date: 20-Oct-1994 #sequence\_revision 15-Feb-1996 #text\_change 15-Feb-1996  
C;Accession: S43383  
R;Qi, S.Y.; Li, Y.; O'Connor, C.D.  
Biochem. J. 238, 711-719, 1994  
A;Title: The region around residue 115 of human bactericidal/permeability-increasing protein of a gene coding for the active domain and characterization of recombinant proteins.  
A;Reference number: S43383  
A;Accession: S43383  
A;Molecule type: DNA  
A;Residues: 1-250 <QIS>

Query Match 51.4%; Score 1288; DB 4; Length 250;  
Best Local Similarity 100.0%; Pred. No. 2e-92;  
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 VNFQVVRISQKGLDYASQGTAAALQKELKRIKIPDYSDFKIKHLGKHGHSFYSDIRE 91  
Db 2 VNFQVVRISQKGLDYASQGTAAALQKELKRIKIPDYSDFKIKHLGKHGHSFYSDIRE 61  
Qy 92 FQLPSSQISWPNVGLKFSISNANIKISGKWAQKRFKLVKSGNFDLSIEGMSISADLKL 151  
Db 62 FQLPSSQISWPNVGLKFSISNANIKISGKWAQKRFKLVKSGNFDLSIEGMSISADLKL 121  
Qy 152 SNPTSGKPTITCSSCSSHINSVHVHISKSVGWLIIQLFHKKIESALRNKNSQVCEKVTN 211  
Db 122 SNPTSGKPTITCSSCSSHINSVHVHISKSVGWLIIQLFHKKIESALRNKNSQVCEKVTN 181  
Qy 212 SVSSKLOPYFQTLPVMTKIDSVAGINYLVAIPATTAETLDVQMKGEFYSNHNPPPP 271  
Db 182 SVSSKLOPYFQTLPVMTKIDSVAGINYLVAIPATTAETLDVQMKGEFYSNHNPPPP 241  
Qy 272 PPVMEFPAA 280



Db	67	KXAVGRQGEYFHSLEIQSQLRGSSLKPLPGRGLSLISDSSISVRGKWKVRRSPVKLH	126
Qy	133	GNFDLSTEGHSISADLKLGNSPTSGKPTITCSSCSHNSVHVHISKSKVGLIQLPHKK	192
Db	127	GSPDLVKSVTISVDLLGVDP--SERPTVTASGCSNRIRDLRHVS--GNVGLNLNLFHQ	184
Qy	193	IESALRNKMSQVCEKVTNSVSKLQPYFOTLPVMTKIDSVAGINYLGLVAPPATTAEILD	252
Db	185	IESKLOKVLBSKICEMIQKSVTSDLOPYLOTLPVTADITILGIDISLVAAPOAKAQTL	244
Qy	253	VQMKGEFYSNNHNPFPAPVMEFFPAADHDMVYLGLSDYFFNTAGLVQEAQVLMKTLR	312
Db	245	VMFKEGFENRHSPTVTPPTMSLPEDSKQMVYFAISDQAFNIATRVHQAGYLNFTIT	304
Qy	313	DDMIPKESKRLTTKFGTLPPEVAKFPMNKIQIHVSASTPHLSVQPTGLTFYPAVDV	372
Db	305	DDMLPPDSNIRLNKAFRPTPLITRKYPDMNLELGTVVSAFLNVSPGNLSLAPQMEI	364
Qy	373	QAFVLPNSSLASFLIGMHTTGSMEVSAESNRLVGELKDLRLLELKHNSNIGFPFVELL	432
Db	365	EGFVLPSSARESVFRLGVTVNVFVSLTFDNSKVTGMHPEKAQVRLIESKVGWNVNLF	424
Qy	433	QDIMNYIVILVPRVNEKLQGFPLPTPARVOLYNNVLQPHQNFLLFGADVVY	486
Db	425	QAFNLNLSLYPDVNDLAKGFPLPLPRRIKLHDLDFQIHKNFLYLGANVOY	478
RESULT 7			
B35943			
lipopolysaccharide-binding protein - rabbit			
C;Species: Oryctolagus cuniculus (domestic rabbit)			
C;Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 09-Jul-2004			
C;Accession: B35843; A46553			
R;Schumann, R.R.; Leong, S.R.; Flaggs, G.W.; Gray, P.W.; Wright, S.D.; Mathison, J.C.; T			
Science 249, 1429-1431, 1990			
A;Title: Structure and function of lipopolysaccharide binding protein.			
A;Reference number: A35843; MUID:90385281; PMID:2402637			
A;Accession: B35843			
A;Status: preliminary			
A;Molecule type: mRNA			
A;Residues: 1-482 <SCH>			
A;Cross-references: UNIPROT:P17454; GB:M35534; NID:g165467; PIDN:AAA99235.1; PID:g165468			
R;Tobias, P.S.; Soldau, K.; Ulevitch, R.J.			
J. Exp. Med. 164, 777-793, 1985			
A;Title: Isolation of a lipopolysaccharide-binding acute phase reactant from rabbit seru			
A;Reference number: A46553; MUID:86306528; PMID:2427635			
A;Accession: A46553			
A;Molecule type: protein			
A;Residues: 27-55,'XG','58-62','F',64-65 <TOB>			
C;Superfamily: lipopolysaccharide-binding protein			
C;Keywords: acute phase			
Query Match 39.3%; Score 985.5; DB 2; Length 482;			
Best Local Similarity 40.9%; Pred. No. 1.6e-68;			
Matches 193; Conservative 103; Mismatches 171; Indels 5; Gaps 3;			
Qy	16	VSLMVLVAIGTAVTAANPGVVVIRISQGLDYASQQGTAALQKELRIKIPDYSDSKIK	75
Db	14	LSLLIAAAPGALGT---NPLGITRITDKGLEAYAREGLALQRLLEVTLPDSGDGFRIK	70
Qy	76	HLKGHYSFYSDMIREFQLPSSQISWMPNVGLKFSISNANIKSGKWKAKRFLKMSGNF	135
Db	71	HFGRAQYKFSYLSKLPREFELLRGTLURPLPGQGLSDISDAIHVKGSGWKVRKAFRLKNSP	130
Qy	136	DLSTEGHSISADLKLGNSPTSGKPTITCSSCSHNSVHVHISKSKVGLIQLPHKKIES	195
Db	131	DLVYKGLTISVHLVLSGE--SSGRPTVITSSCSSDIQNVELDI--EGDLEELNLLQSQIDA	188
Qy	196	ALRNKMSQVCEKVTNSVSKLQPYFOTLPVMTKIDSVAGINYLGLVAPPATTAEILDVQM	255
Db	189	RLRVLESKICQRIEEAVTAHLQYLOTLPVTTOIDSFAGIDYSLMEAPRATGMLDVMF	248
Qy	256	KGEFYSNNHNPFPAPVMEFFPAADHDMVYLGLSDYFFNTAGLVQEAQVLMKTLRDDM	315

Db	249	KGEIPLDHRSPVDFLAPAMNLPASHRMVYFISDYVENTASLAYHKSGYWNFSITDAM	308
Qy	316	IPKESKRLTTTKFFGCTFLPEVAKKPNMKIQIHVSASTPHLSVQPTGLTFYPAVDVQAF	375
Db	309	VFADLNIRRTTKTSFRFPVFLLANLYNNMLELQGTVTNVSQNLNSTENLEEEPEMDIEAL	368
Qy	376	AVLPNSSLASFLIGHMHTTGSMEVSAESNRLVGELKDLRLLELKHNSNIGPFPFVELLODI	435
Db	369	VVLPSAREPVRGLGVATNVVSATLITNTRKITGFLKPGRLQVELKESKVGGENVELLEAL	428
Qy	436	MNYIVILVLPVNEKLQGFPLPTPARVOLYNNVLQPHQNFLLFGADVVYK	487
Db	429	LNYYILNLYPKVNEKLAHRFPLEPLRLHTQLYDILLQTHENFLLVGANIQYR	480
RESULT 8			
A53533			
phospholipid transfer protein precursor - human			
N;Alternate names: lipid transfer protein II; PLTP			
C;Species: Homo sapiens (man)			
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004			
C;Accession: A53533			
R;Day, J.R.; Albers, J.J.; Lofton-Day, C.E.; Gilbert, T.L.; Ching, A.F.T.; Grant, F.J.; C			
J. Biol. Chem. 269, 9388-9391, 1994			
A;Title: Complete cDNA encoding human phospholipid transfer protein from human endothel			
A;Reference number: A53533; MUID:94179366; PMID:8132678			
A;Accession: A53533			
A;Status: preliminary			
A;Molecule type: mRNA			
A;Residues: 1-493 <DAY>			
A;Cross-references: UNIPROT:P55058; GB:L26232; NID:g468325; PIDN:AAA36443.1; PID:g468326			
C;Genetics:			
A;Gene: GDB:PLTP			
A;Cross-references: GDB:340911; OMIM:174245			
A;Map position: 20pter-20qter			
C;Superfamily: lipopolysaccharide-binding protein			
C;Keywords: glycoprotein; phosphoprotein			
F;1-17/Domain: signal sequence #status predicted <SIG>			
F;18-493/Product: phospholipid transfer protein #status experimental <MAT>			
Query Match 18.5%; Score 465; DB 2; Length 493;			
Best Local Similarity 26.9%; Pred. No. 4e-28;			
Matches 124; Conservative 95; Mismatches 214; Indels 28; Gaps 10;			
Qy	34	PGVVVIRISQGLDYASQQGTAALQKELRIKIPDYSDSKIKHLGKHG--YSFYSMDIRE	91
Db	20	PGCKIRVTSKALELVKQEGRLRPLEQELETITIPDLRGK-----EGHFYINISEVKVTE	72
Qy	92	FQLPSSQISWMPNVNVLKFSISNANIKISGKWKAKRFLKMSGNFDSLSEIGMSISADLKLG	151
Db	73	LQUTSSELDFOPOQOELMLQITNASLGLRFRRLYWFYDGGYINASAEGVSIRTGLELS	132
Qy	152	SNPTSGKPTITCSSCSHNSVHVHISKS--KVGWLIQLFHKKIESALRNKMSQVCEKV	209
Db	133	RDP--ACRMKYSNVSCQASVSRMHAFFGTFKVVYDFLSTF---ITSGMRFLNQOICPVL	188
Qy	210	TNSVSKLQPYFOTLPVMTKIDSVAGINYLGLVAPPATTAEITLDVQMKGEFYSNNHN---	266
Db	189	YHAGTVLLNSLLDTPVRSVSDVLGIDYSIMKDPVASTNSLNDMDPFGAFPFITERWNSL	248
Qy	267	PPFPAPVMEFFPAADHDMVYLGLSDYFFNTAGLVQEAQVLMKTLRDDMIPKESKRLTT	326
Db	249	PNRAVEPQOQ---EERMVYAFSEFFSDSMESYFRAGALQILLVGDVKVPHDLMLRA	305
Qy	327	KFFGTFL---PEVAKFPMNKIQIHVSASTPHLSVQPTGLTFYPAVDVQAFVLPNSSL	383
Db	306	TYFGSIVLLSPAIDS--PLKLELRVLA--PPRCTIKPSGTTISVTSVATIALVPPDQPE	361
Qy	384	ASLFLTMHTTGSMEVSAESNRLVGELKDLRLLELKHNSNIGPFPFVELLODIWNYIVPL	443
Db	362	VQLSSMTMDARLSAKMALRGKALRTQLDLRRFRFRIYNNHSALESALILPQAPLTKMLQIG	421





Query Match 11.8%; Score 295; DB 2; Length 493;  
Best Local Similarity 23.7%; Pred. No. 6.2e-15;  
Matches 116; Conservative 92; Mismatches 243; Indels 38; Gaps 16;

QY 17 SLAVLVVAIGTAVTAAV-----NPGVVVRISSQGLDYASQQGTAALQKELKRIKIPDYSDSF 72  
DB 5 TVITALLGNAHACSKGTSHEAGIVCRITKPAALLVLNHNHETAKVIQTAFORASPDITGEK 64  
QY 73 KIKHLKGHYFSFMSDIREPQLPSSQISMPVNVGLKFSISNANIKISGKWK---AQKREL 129  
DB 65 AMLLGQVKGKLNHIQIHLHSIASSQVELVEAKSIDVSIQNVSVVFGTKLKYGYTTANWL 124  
QY 130 KMGSNFDLSIEGMSISADLKLGNPT--SKPTITCSSCSHSHNSVHVHI-SKSKVGLWI 186  
DB 125 GIDQSIDFEIDS---AIDLQINTQLTCDSGRVRTDAPDCVLSFKHLLHLQGEREPGWIK 181  
QY 187 QLFHKHTESALRNKNSQVEKVTNSVSKLPYFQTLPMVKIDSVAGINYGLVAPPAT 246  
DB 182 QLEFTNFISFTKLVLKGLQIKCKEI-NVISNIMADFVQTRAASIIISDGDIGVDISLTGDPVI 240  
QY 247 TAETLDVQMGKEGFYSNHNHP---PPAPPVMEFPAADRMVYLVGLSDYFFNTAGLVYQE 303  
DB 241 TASVLESHHKGHFYKYNVSEDLPLPTSPFLL---GDSRLYFWFSRVFHSIAKVAQ 296  
QY 304 AGVKMLTRDDMPKESKFLITTKFFGT---FLPEVAKFPNNMKIQITHVSASTPPLHSVQ 360  
DB 297 DGRMLSLMGD---EPKAVLETWGFNTNQEIHQEVVGGFPS-QAQVTVHCLKMPKISQ 351  
QY 361 PTGLTFTFPADVQAFVLPNS--SLASFLIGHMTTGSMEVSAESNRLVGLKLDRLLE 418  
DB 352 NKGVVNVSSVMVFKPLPRPDQOHSVAYTFEEDIVTT--VQASYSKKKFLLSL-LDFQITP 408  
QY 419 LKHSNIGPPFVELLODMNVIPILVPLRYNEKLOGF-PLPTPARVQLXNVV---LQPH 474  
DB 409 KTVSNLTSESSESISQSLQSMITAVGIPEVNSRLVVFTALMNSKGVSLFDINPEIIR 468  
QY 475 QNFLLFGAD 483  
DB 469 DGFLLQMD 477

RESULT 12  
A53176  
cholesteryl ester transfer protein - crab-eating macaque  
C/Species: Macaca fascicularis (crab-eating macaque)  
C/Date: 12-May-1994 #sequence\_revision 12-May-1994 #text\_change 07-May-1999  
C/Accession: A53176  
R/Pape, M.E.; Rehberg, E.F.; Marotti, K.R.; Melchior, G.W.  
Arterioscler. Thromb. 11, 1759-1771, 1991  
A/Title: Molecular cloning, sequence, and expression of cynomolgus monkey cholesteryl ester transfer protein levels  
A/Reference number: A53176; MUID:92031355; PMID:1931878  
A/Accession: A53176  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-493 <PAP>  
A/Cross-references: GB:M86343

Query Match 11.2%; Score 282; DB 2; Length 493;  
Best Local Similarity 23.8%; Pred. No. 6.4e-14;  
Matches 111; Conservative 89; Mismatches 233; Indels 34; Gaps 15;

QY 35 GVVVRISSQGLDYASQQGTAALQKELKRIKIPDYSDFKIKHLKGHYFSYDWDIREFQL 94  
DB 27 GIVCRITKPAALLVLNHNHETAKVIQSAFORANYPNITGKAMMLIGQVKYGLHNIQIHLSI 86  
QY 95 PSSQISMPVNVGLKFSISNANIKISGKWK---AQKRELKMGSNFDLSIEGMSISADLKL 151  
DB 87 ASSRVELVEAKSIDVSIQNVSVFEGTKLVGYTTAWGLGIDQSDVDFEIDS---AIDLQIN 143  
QY 152 SNPT--SKPTITCSSCSHSHNSVHVHI-SKSKVGLWLIQLFHKHTESALRNKNSQVCEK 208  
DB 144 TQITCDSGRVRTDAPDCVLSFKHLLHLQGEREPGWI KOLFTNFIPTFLKVLKGLQIKCKE 203



Db 401 SANLSVALRTEAKAVSNLTESRSLSQSSLRSLATVGIPEVMGRLEVAFTALNMNSKGLD 460  
 Qy 466 LYNVV 470  
 Db 461 LFEII 465

RESULT 14  
 S17447  
 Probable ligand-binding protein RY2G5 - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 13-Jan-1995 #sequence\_revision 22-May-1998 #text\_change 05-Nov-1999  
 C:Accession: S17447  
 R:Dear, T.N.; Boehm, T.; Keverne, E.B.; Rabbitts, T.H.  
 EMBO J. 10, 2813-2819, 1991  
 A:Title: Novel genes for potential ligand-binding proteins in subregions of the olfactory  
 A:Reference number: S17447; PMID:92007724; PMID:1915264  
 A:Accession: S17447  
 A:Molecule type: mRNA  
 A:Residues: 1-470 <DEA>  
 A:Cross-references: EMBL:X60660; NID:g57731; PIDN:CAA43067.1; PID:g57732  
 A:Experimental source: olfactory mucosa  
 C:Genetics:  
 A:Gene: RY2G5  
 C:Keywords: olfaction

Query Match 10.4%; Score 261.5; DB 2; Length 470;  
 Best Local Similarity 22.4%; Pred. No. 2.3e-12; Indels 27; Gaps 11;  
 Matches 90; Conservative 80; Mismatches 204;

Qy 89 IREFOLPSSQISMVNVGLKFSISNANIKISGKWKAKRFLKMSGNFSLSEIEMGMSISADL 148  
 Db 84 IVELTLPRVSVRLPGVGYLSL-YTRVAINGK-----SLIGFLDIAVE-VNITAKV 133

Qy 149 KLGSNPTSGKPTITCSSCSHNSVHVHISKSKVGLIQLFHKKIESALRNKMSQVCEK 208  
 Db 134 RLTMRT-GYPLRVIERCDTLGGIKVKLLR---GLLPNLVNLVNRVLNVLPLDLC-P 188

Qy 209 VTNVSSSKLQPYFQTLPVMTKIDSVAGINYLVAAPPATTAEITLDVQMK-----GEFVS 261  
 Db 189 IVDVVLGLVNDQLGLVDSLVPIGLIGSVQYTFSSPLVTGTFELEDLNLVGEAGDLD 248

Qy 262 ENHNHPPPPAPPVM-EFFAAHDM-VYLGSLDYFFNTAGLVYQEAGVLMKTLRDDMIKPE 319  
 Db 249 YPLGRPAMLPRQMPFLPMDNTNSQLAISANFLSVLTMQLKQGLDIDITDGMF--E 306

Qy 320 SKFRLTTFKFFGTFLEVAKKFPMK-IQIHVSASTPPHLSVQPTGLTFYPADVQVAFVL 378  
 Db 307 DLPLTTSTLGLALPKVFOQYPSRPLTIRIQVNPPTVTLOKDKALVKVFATSEVVVSQ 366

Qy 379 PNSSLASFLIGHMTTGSMEVSAENRVLGELKLDRLLELKHNSIGPPVVELLODMNY 438  
 Db 367 PNDVETICLDVDVLDLASFSVEGKLMIDAKLTKSLNLTSGNVDVFNLEMLVEK 426

Qy 439 IVPILVLRVNEKLOKGFPLTPARVQLNVNVLQPHQNFLL 479  
 Db 427 IFDLAFMPANNAILGSGVPLKILNIDFSNADIVLEDLV 467

RESULT 15  
 S17448  
 Probable ligand-binding protein RY3 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999  
 C:Accession: S17448  
 R:Dear, T.N.; Boehm, T.; Keverne, E.B.; Rabbitts, T.H.  
 EMBO J. 10, 2813-2819, 1991  
 A:Title: Novel genes for potential ligand-binding proteins in subregions of the olfactory  
 A:Reference number: S17447; PMID:92007724; PMID:1915264  
 A:Accession: S17448  
 A:Status: preliminary  
 A:Molecule type: mRNA

A:Residues: 1-473 <DEA>  
 A:Cross-references: EMBL:X60658; NID:g57733; PIDN:CAA43065.1; PID:g57734

Query Match 9.4%; Score 234.5; DB 2; Length 473;  
 Best Local Similarity 21.8%; Pred. No. 2.9e-10;  
 Matches 109; Conservative 88; Mismatches 229; Indels 75; Gaps 18;

Qy 13 PRVSLMVLVAIGTAVTAANVP-GVVVRISOKGLDYASQ---GTAALQKELKRIK---- 64  
 Db 3 PGVYALLMLGLATPCGLLETVGTARIDKDEYKAQNSLVGGPILQNLVLTVTYSNQ 62

Qy 65 -----IPDYSDSEFKIKHLGKGYHYSFYSMDIREFQLPSSQISMVNVGLKFSI 111  
 Db 63 GLLGAGLLGGGGLSLVGLFSLVEELSG-----LKIEELTLFVSKILPGVGVQVLSL 116

Qy 112 SNANIKISGKWKAKRFLKMSGNFSLSEIEMGMSISADLKGNSNPTSGKPTITCSSCSHIN 171  
 Db 117 -HTKVSLLHSGS-----PLVGLLQLAEE-VNVSSKVALGMSR-RGTPIILIKRC-----N 162

Qy 172 SVHVHISKSKVGLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPVMTKID 231  
 Db 163 TLLGHISLTS-GLLPTPIFGLVEQTLCKVLPGLLC-PVDSVLVSVNELLGATLSLVLG 220

Qy 232 SVAGINYLVAAPPATTAEITLDVQMKGEFYSNHNHP--PPAPPVMEPPAA----- 280  
 Db 221 PLGSVEFTLATPLISNOYIELDI-----NPIVKSIAQDVDPKPRLPVMPPK 270

Qy 281 --HDMVVLGLSDYFFNTAGLVYQEAGVLMKTLRDDMIKPKSKRLTTKFFGTFLEVAK 338  
 Db 271 EDHTSQVTVPL--YLFNTVFGLLQTNGALDLDITPEMVR--NIFLTITDLAALAPEALG 326

Qy 339 KPP---NMKIQIHVSASTPPHLSVQPTGLTFYPADVQVAFVLPNSSLASFLIGHMTTG 395  
 Db 327 KLPPCQHLLSLRVNKS--PMILLQNKVTVSIPVTIHLSSVPOQTPTVALFQMGVMTL 384

Qy 396 SMEVSAENRVLGELKLDRLLELKHNSIGPPVVELLODMNYIVPILVLRVNEKLOK 455  
 Db 385 NAHLVPSTTKLHISLSLERLTVQLASSFSQFDSARLEELSDVVVRAAYMQKLNHELVG 444

Qy 456 PPLTPARVQLNVNVLQPHQN 476  
 Db 445 IPLPKILNVNFAVSVDVVIEN 465

Search completed: October 21, 2005, 11:31:47  
 Job time : 41.7407 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2005, 11:22:43 ; Search time 64.7154 Seconds  
(without alignments)  
1455.954 Million cell updates/sec

Title: US-10-629-516-2\_COPY\_10\_193

Perfect score: 943

Sequence: 1 CNAPRWVSLVLAIGTAVT.....HVHISKVGVWLIQLFHKKI 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	943	100.0	483	1	BPI_HUMAN	P17213 homo sapien
2	939	99.6	487	2	Q81W58	Q81W58 homo sapien
3	688	73.0	179	2	Q9GK39	Q9GK39 macaca mula
4	596.5	63.3	482	1	BPI_BOVIN	P17453 bos taurus
5	567.5	60.2	482	2	Q6AXU0	Q6AXU0 rattus norv
6	554.5	58.8	483	2	Q67E05	Q67E05 mus musculus
7	554.5	58.8	486	2	Q8BSF3	Q8BSF3 mus musculus
8	518.5	55.0	178	2	Q9GK40	Q9GK40 oryctolagus
9	506.5	53.7	445	1	BPI_RABIT	Q28739 oryctolagus
10	448	47.5	481	1	LBP_MOUSE	Q81805 mus musculus
11	429	45.5	477	2	Q8TCF0	Q8TCF0 homo sapien
12	429	45.5	481	1	LBP_HUMAN	P18428 homo sapien
13	428	45.4	481	1	LBP_RAT	Q63313 rattus norv
14	394	41.8	476	2	Q6GLX0	Q6GLX0 xenopus lae
15	357.5	37.9	482	1	LBP_RABIT	P17454 oryctolagus
16	312.5	33.1	473	2	Q773Q8	Q773Q8 gadus morhu
17	312.5	33.1	473	2	Q773Q9	Q773Q9 gadus morhu
18	312.5	33.1	473	2	Q804Q9	Q804Q9 cyprinus ca
19	312	33.1	473	2	Q8JFX3	Q8JFX3 oncorhynch
20	311.5	33.0	473	2	Q8JFX4	Q8JFX4 oncorhynch
21	222.5	23.6	477	2	Q81729	Q81729 crassostrea
22	197.5	20.9	507	1	BPI2_HUMAN	Q8N1Q6 homo sapien
23	186.5	19.8	509	1	BPI2_MOUSE	Q8C186 mus musculus
24	172.5	18.3	493	1	PLTP_MOUSE	P55065 mus musculus
25	169	17.9	493	1	PLTP_HUMAN	P55058 homo sapien
26	166	17.6	496	2	Q8WMN7	Q8WMN7 sus scrofa
27	156	16.5	48	2	Q864W2	Q864W2 sus scrofa
28	153.5	16.3	503	2	Q8WNG5	Q8WNG5 oryctolagus
29	153.5	16.3	503	2	Q95JG0	Q95JG0 oryctolagus
30	148	15.7	483	2	Q6GIU4	Q6GIU4 xenopus lae
31	141	15.0	486	2	Q6DEI0	Q6DEI0 brachydanio

RESULT 1

ID	BPI_HUMAN	STANDARD	PRT	483 AA
AC	P17213-Q9BY29; Q9H1L2; Q9H1M8; Q9H203; Q9UD65;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DE	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Bactericidal permeability-increasing protein precursor (BPI) (CAP 57).			
GN	Name=BPI;			
OS	Homo sapiens (Human);			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 28-64.			
RX	MEDLINE=89255455; PubMed=272846;			
RA	Gray P.W., Flagg G., Leong S.R., Gumina R.J., Weiss J., Ooi C.E.,			
RA	Elsbach P.;			
RT	"Cloning of the cDNA of a human neutrophil bactericidal protein.			
RT	Structural and functional correlations.";			
RL	J. Biol. Chem. 264:9505-9509(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94292492; PubMed=7517398;			
RA	Wilde C.G., Seilhamer J.J., McGrogan M., Ashton N., Snable J.L.,			
RA	Lane J.C., Leong S.R., Thornton M.B., Miller K.L., Scott R.W.;			
RT	"Bactericidal/permeability-increasing protein and lipopolysaccharide			
RT	(LPS)-binding protein. LPS binding properties and effects on LPS-			
RT	mediated cell activation.";			
RL	J. Biol. Chem. 269:4741-4746(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND VARIANT ALA-12.			
RA	Xu J., Wang H.;			
RT	"Cloning of cDNA of human bactericidal/permeability-increasing			
RT	protein.";			
RL	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A., AND VARIANTS ALA-12 AND GLU-212.			
RX	MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;			
RA	Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,			
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,			
RA	Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,			
RA	Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,			
RA	Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,			
RA	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,			
RA	Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,			
RA	Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,			
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,			
RA	Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,			
RA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,			
RA	Huckle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,			
RA	Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,			
RA	Lehvaeslaho M.H., Leversha M.A., Lloyd C., Lloyd D., Lovell J.D.,			
RA	Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,			

32	139.5	14.8	485	2	Q9BG59	Q9BG59 tupaia glis
33	130.5	13.8	493	1	CETP_HUMAN	P11597 homo sapien
34	129.5	13.7	489	1	YSV5_CABEL	Q10011 caenorhabdi
35	129.5	13.7	497	1	CETP_RABIT	P22687 oryctolagus
36	120.5	12.8	493	1	CETP_MACFA	P47896 macaca fasc
37	113.5	12.0	515	2	Q8VYC2	Q8VYC2 arabidopsis
38	112	11.9	42	2	Q9N0U2	Q9N0U2 sus scrofa
39	110	11.7	551	2	Q93796	Q93796 caenorhabdi
40	110	11.7	573	2	Q6RV01	Q6RV01 caenorhabdi
41	105	11.1	22	2	Q9UCT4	Q9UCT4 homo sapien
42	103	10.9	458	1	BPI_L_HUMAN	Q8N4F0 homo sapien
43	103	10.9	458	2	Q6UMN3	Q6UMN3 homo sapien
44	103	10.9	458	2	Q6ZME0	Q6ZME0 homo sapien
45	102	10.8	606	2	Q18869	Q18869 caenorhabdi

ALIGNMENTS

RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Rangeay H.,  
RA Rice C.M., Ross M.T., Scott C.E., Shra H.K., Shownkeen R., Sims S.,  
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
RA Rogers J.,  
RA "The DNA sequence and comparative analysis of human chromosome 20.";  
RL Nature 414:865-871(2001).  
RN [5]  
RP SEQUENCE OF 28-42.  
RX MEDLINE=88033057; PubMed=3667613;  
RA Ooi C.E., Weiss J., Elsbach P., Frangione B., Mannion B.;  
RT "A 25-kDa NH2-terminal fragment carries all the antibacterial  
RT activities of the human neutrophil 60-kDa bactericidal/permeability-  
RT increasing protein.";  
RL J. Biol. Chem. 262:14891-14894(1987).  
RN [6]  
RP SEQUENCE OF 28-47.  
RX MEDLINE=89315847; PubMed=2501794;  
RA Gabay J.E., Scott R.W., Campanelli D., Griffith J., Wilde C.,  
RA Marra M.N., Seeger M., Nathan C.F.;  
RT "Antibiotic proteins of human polymorphonuclear leukocytes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:5610-5614(1989).  
RN [7]  
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).  
RX MEDLINE=97334442; PubMed=9189532; DOI=10.1126/science.276.5320.1861;  
RA Beamer L.J., Carroll S.F., Eisenberg D.;  
RT "Crystal structure of human BPI and two bound phospholipids at 2.4-A  
RT resolution.";  
RL Science 276:1861-1864(1997).  
CC -1- FUNCTION: The cytotoxic action of BPI is limited to many species  
CC of Gram-negative bacteria; this specificity may be explained by a  
CC strong affinity of the very basic N-terminal half for the  
CC negatively charged lipopolysaccharides that are unique to the  
CC Gram-negative bacterial outer envelope.  
CC -1- SUBCELLULAR LOCATION: Membrane-associated in polymorphonuclear  
CC leukocytes (PMN) granules.  
CC -1- TISSUE SPECIFICITY: Restricted to cells of the myeloid series.  
CC -1- DOMAIN: The N-terminal region may be exposed to the interior of  
CC the granule, whereas the C-terminal portion may be embedded in the  
CC membrane. During phagocytosis and degranulation, proteases may be  
CC released and activated and cleave BPI at the junction of the N-  
CC and C-terminal portions of the molecule, providing controlled  
CC release of the N-terminal antibacterial fragment when bacteria are  
CC ingested.  
CC -1- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP  
CC family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; J04739; AAA51841.1; ALT INIT.  
CC EMBL; AF322588; AAG42844.1; -  
CC EMBL; AL359555; CAC13043.1; -  
CC EMBL; AL499625; CAC27350.1; -  
CC EMBL; AL391692; CAC10453.1; -  
CC PDB; 1BP1; X-ray; @=28-483.  
CC PDB; 1EWF; X-ray; @=28-483.  
CC Genew; HGNC:1095; BPI.  
CC MIM; 109195; -  
CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
CC InterPro; IPR001124; LBP\_BPI\_CETP.  
CC Pfam; PF01273; LBP\_BPI\_CETP; 1.  
CC Pfam; PF02886; LBP\_BPI\_CETP\_C; 1.

DR SMART; SM00328; BPI1; 1.  
DR SMART; SM00329; BPI2; 1.  
DR PROSITE; PS00400; LBP\_BPI\_CETP; 1.  
KW 3D-structure; Antibiotic; Direct protein sequencing; Glycoprotein;  
KW Polymorphism; Signal; Transmembrane.  
FT SIGNAL 1 27  
FT CHAIN 28 483 Bactericidal permeability-increasing  
FT protein.  
FT SITE 236 241 Cleavage sites for elastase (Potential).  
FT TRANSMEM 365 385 Potential.  
FT VARIANT 12 12 V -> A (in dbSNP:1341023).  
FT VARIANT 192 192 A -> V (in dbSNP:5743509).  
FT VARIANT 212 212 /FTId=VAR\_018402.  
FT VARIANT 212 212 K -> E (in dbSNP:4358188).  
FT CONFLICT 351 351 P -> S (in Ref. 3).  
FT CONFLICT 371 371 F -> L (in Ref. 2).  
FT CONFLICT 400 400 N -> D (in Ref. 3).  
FT CONFLICT 407 407 K -> R (in Ref. 3).  
FT STRAND 32 37  
FT HELIX 38 56  
FT TURN 57 58  
FT STRAND 64 67  
FT STRAND 77 89  
FT STRAND 93 98  
FT TURN 99 101  
FT STRAND 102 122  
FT TURN 123 124  
FT STRAND 125 149  
FT TURN 150 153  
FT STRAND 154 165  
FT STRAND 168 172  
FT HELIX 176 178  
FT HELIX 179 188  
FT TURN 189 189  
FT HELIX 190 211  
FT TURN 212 212  
FT HELIX 213 217  
FT TURN 218 219  
FT STRAND 223 225  
FT STRAND 231 233  
FT STRAND 236 236  
FT STRAND 241 242  
FT STRAND 246 251  
FT STRAND 254 256  
FT STRAND 281 286  
FT HELIX 287 299  
FT TURN 300 301  
FT STRAND 304 308  
FT HELIX 309 311  
FT TURN 314 315  
FT STRAND 321 321  
FT HELIX 322 326  
FT TURN 327 328  
FT HELIX 332 335  
FT TURN 337 338  
FT STRAND 340 346  
FT STRAND 352 356  
FT TURN 357 358  
FT STRAND 359 363  
FT STRAND 365 373  
FT TURN 375 376  
FT STRAND 379 388  
FT STRAND 391 397  
FT STRAND 401 408  
FT STRAND 412 418  
FT HELIX 425 428  
FT HELIX 429 439  
FT TURN 440 440  
FT TURN 441 450  
FT HELIX 452 453  
FT TURN 458 459

```
FT STRAND 460 470
FT TURN 471 472

Query Match 100.0%; Score 943; DB 1; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.7e-75;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNAPRWYSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 60
DB 6 CNAPRWYSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 65
QY 61 DSFKIKHLGKHGHSFYSDMIREFOLPSSQISWPNVGLKFSISNANIKISGKWAQKRF 120
DB 66 DSFKIKHLGKHGHSFYSDMIREFOLPSSQISWPNVGLKFSISNANIKISGKWAQKRF 125
QY 121 KMSGNFDSLSTEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHSHSKVGVLIQLF 180
DB 126 KMSGNFDSLSTEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHSHSKVGVLIQLF 185
QY 181 HKXI 184
DB 186 HKXI 189

RESULT 2
ID Q8IW58 PRELIMINARY; PRT; 487 AA.
AC Q8IW58;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Bactericidal/permeability-increasing protein..
GN Name=BPI;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalicki D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC040955; AAH40955.1; -.
DR HSSP; P17213; 1EWF.
DR GO; GO:0008289; F.lipid binding; IEA.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP; 1.
DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR SMART; SM00328; BPI1; 1.

DR SMART; SM00329; BPI2; 1.
DR PROSITE; PS00400; LBP_BPI_CETP; 1.
SQ SEQUENCE 487 AA; 53880 MW; FE709D9317E5206D CRC64;

Query Match 99.6%; Score 939; DB 2; Length 487;
Best Local Similarity 99.5%; Pred. No. 8.4e-75;
Matches 183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNAPRWYSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 60
DB 10 CNAPRWYSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 69
QY 61 DSFKIKHLGKHGHSFYSDMIREFOLPSSQISWPNVGLKFSISNANIKISGKWAQKRF 120
DB 70 DSFKIKHLGKHGHSFYSDMIREFOLPSSQISWPNVGLKFSISNANIKISGKWAQKRF 129
QY 121 KMSGNFDSLSTEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHSHSKVGVLIQLF 180
DB 130 KMSGNFDSLSTEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHSHSKVGVLIQLF 189
QY 181 HKXI 184
DB 190 HKXI 193

RESULT 3
ID Q9GK39 PRELIMINARY; PRT; 179 AA.
AC Q9GK39;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Bactericidal/permeability-increasing protein (fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OC NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu J., Wang H.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF322587; AAG42843.1; -.
DR HSSP; P17213; 1EWF.
DR GO; GO:0008289; F.lipid binding; IEA.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP; 1.
DR SMART; SM00328; BPI1; 1.
FT NON TER 1
FT NON TER 179 179
SQ SEQUENCE 179 AA; 19772 MW; F1B180A02A38CE63 CRC64;

Query Match 73.0%; Score 688; DB 2; Length 179;
Best Local Similarity 88.2%; Pred. No. 5.1e-53;
Matches 134; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 33 QKGLDYASQOQTAALQKELKRIKIPDYSDFSKIKHLGKHGHSFYSDMIREFOLPSSQISM 92
DB 1 QKGLDYASQOQTAALQKELKRIKIPDYSDFSKIKHLGKHGHSFYSDMIREFOLPSSQISM 60
QY 93 VPNVGLKFSISNANIKISGKWAQKRFKMSGNFDSLSTEGMSISADLKLGSNPTSGKPTI 152
DB 61 VPNVGLKFSISNANIKISGKWAQKRFKTSNFDLSVGGVSVISADLKLGSNPTSGKPTI 120
QY 153 TCSCSSHNSVHVHSHSKVGVLIQLFHKXI 184
DB 121 SCSCSSHNSVHVHSHSKVGVLIQLFHKXI 152

RESULT 4
BPI_BOVIN
ID BPI_BOVIN STANDARD; PRT; 482 AA.
AC P17453;
```

DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Bactericidal permeability-increasing protein precursor (BPI).  
 GN Name=BPI;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Bone marrow;  
 RX MEDLINE=90272418; PubMed=2349103;  
 RA "Leong S.R., Camerato T.;  
 RT "Nucleotide sequence of the bovine bactericidal permeability  
 RL Nucleic Acids Res. 18:3052-3052(1990).  
 CC -I- FUNCTION: The cytotoxic action of BPI is limited to many species  
 CC of Gram-negative bacteria; this specificity may be explained by a  
 CC strong affinity of the very basic N-terminal half for the  
 CC negatively charged lipopolysaccharides that are unique to the  
 CC Gram-negative bacterial outer envelope.  
 CC -I- SUBCELLULAR LOCATION: Membrane-associated in polymorphonuclear  
 CC Leukocytes (PMN) granules (By similarity).  
 CC -I- TISSUE SPECIFICITY: Restricted to cells of the myeloid series (By  
 CC similarity).  
 CC -I- DOMAIN: The N-terminal region may be exposed to the interior of  
 CC the granule, whereas the C-terminal portion may be embedded in the  
 CC membrane. During phagocytosis and degranulation, proteases may be  
 CC released and activated and cleave BPI at the junction of the N-  
 CC and C-terminal portions of the molecule, providing controlled  
 CC release of the N-terminal antibacterial fragment when bacteria are  
 CC ingested (By similarity).  
 CC -I- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP  
 CC family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X52563; CAA36797.1; -;  
 DR PIR; S10180; S10180.  
 DR HSP; P17213; IEWF.  
 DR InterPro; IPR001124; LBP\_BPI\_CETP.  
 DR Pfam; PF01273; LBP\_BPI\_CETP\_1.  
 DR Pfam; PF02886; LBP\_BPI\_CETP\_C; 1.  
 DR SMART; SM00328; BPI1; 1.  
 DR SMART; SM00329; BPI2; 1.  
 DR PROSITE; PS00400; LBP\_BPI\_CETP; 1.  
 DR Antibiatic; Glycoprotein; Membrane; Signal.  
 FT SIGNAL 1 26  
 FT CHAIN 27 482 Bactericidal permeability-increasing  
 FT protein.  
 FT SITE 235 240  
 FT CARBOHYD 62 62 Cleavage sites for elastase (Potential).  
 FT CARBOHYD 303 303 N-linked (GLNAC. .) (Potential).  
 FT CARBOHYD 375 375 N-linked (GLNAC. .) (Potential).  
 FT CARBOHYD 389 389 N-linked (GLNAC. .) (Potential).  
 FT CARBOHYD 463 463 N-linked (GLNAC. .) (Potential).  
 FT SEQUENCE 482 AA; 53432 MW; DD7D59AE785BC42D CRC64;  
 Query Match 63.3%; Score 596.5; DB 1; Length 482;  
 Best Local Similarity 63.2%; Pred. No. 2e-44;  
 Matches 115; Conservative 29; Mismatches 37; Indels 1; Gaps 1;  
 QY 3 APRVSLMLVLAIGTAVTAANPGVVVRISQKGLDYASQOQTAAALQKELKRIKIPYSDS 62  
 DB 8 ARRWATLVLAALGTAVT-TTNPQIVARITQKGLDYACQOQGVLTQLQKELKITIPNPSGN 66

QY 63 FKIKHLGKGYSPYSMDIREFQLPSSQISMPVNVGLKFSISNANIKISGKWKAKRFLKM 122  
 DB 67 FKIKYLGKQYFFSVIOGFNLPSNQIRPLPKDGLDLSDIRDSIKIRGKWKAKRQFIKL 126  
 QY 123 SGNFDLSIEGMSISADKLGSNPTSGKPTTICSSSCSHSHSVHSHSKSVGLWLIQLFHK 182  
 DB 127 GGNFDLSVSGISILAGNLGYDPASGHSTVTCSSCSGGINTVRIHISGSLGLWLIQLFRK 186  
 QY 183 KI 184  
 DB 187 RI 188  
 RESULT 5  
 Q6AXUO PRELIMINARY; PRT; 482 AA.  
 ID Q6AXUO;  
 AC Q6AXUO;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Bactericidal/permeability-increasing protein.  
 GN Name=Bpi;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zerborg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalón D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Faley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RA Director MGC Project;  
 RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC079318; AAH79318.1; -;  
 DR GO; GO:0008289; Filipid binding; IEA.  
 DR InterPro; IPR001124; LBP\_BPI\_CETP.  
 DR Pfam; PF01273; LBP\_BPI\_CETP\_1.  
 DR Pfam; PF02886; LBP\_BPI\_CETP\_C; 1.  
 DR SMART; SM00328; BPI1; 1.  
 DR SMART; SM00329; BPI2; 1.  
 SQ SEQUENCE 482 AA; 53751 MW; 269591C4C2F5A6D1 CRC64;

Query Match 60.2%; Score 567.5; DB 2; Length 482;  
 Best Local Similarity 59.6%; Pred. No. 7.6e-42;  
 Matches 109; Conservative 29; Mismatches 44; Indels 1; Gaps 1;  
 QY 2 NAFVSLMLVLAIGTAVTAANPGVVVRISQKGLDYASQOQTAAALQKELKRIKIPYSD 61  
 DB 7 NVKWSLLALTAIVGTALTAATDPGFVARISQKGLDFVCOESMVLEQLKELLAISIPFSG 66

QY 62 SFKIKHLGKHGHSFFYSMDIRFQIPSSQISWPNVGLKFSISNANIKISGKWKAQKRFLK 121

DB 67 DFKIKHLGKGTVEFFYSMAVEGFHIPDPQIKLLPSDGLQLSITGSASIKISGRWKYRKNILK 126

QY 122 MSGNFDLSIEGMSISADILKLGSNPTSGKPTTICSSCSHNSVHVHISKSKVGMILQLFPH 181

DB 127 ASGNFQLSIOGVSIIADILGNDP-SGRITITCDSHNSVRIKVSGLGMLGWLIRLPH 185

QY 182 KKI 184

DB 186 RKI 188

RESULT 6

Q67E05

ID Q67E05 PRELIMINARY; PRT; 483 AA.

AC Q67E05;

DT 25-OCT-2004 (TREMBLrel. 28, Created)

DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)

DE Bactericidal/permeability-increasing protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxId:10090;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=Swiss Webster;

RC Bingle C.D., Craven J.;

RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY363993; AA013289.1; -.

DR InterPro; IPR001124; LBP\_BPI\_CETP.

DR Pfam; PF01273; LBP\_BPI\_CETP; 1.

DR Pfam; PF02886; LBP\_BPI\_CETP\_C; 1.

DR SMART; SM00328; BPI1; 1.

DR SMART; SM00329; BPI2; 1.

SQ SEQUENCE 483 AA; 53940 MW; 4AA2D48095C52B74 CRC64;

Query Match 58.8%; Score 554.5; DB 2; Length 483;

Best Local Similarity 57.9%; Pred. No. 1.1e-40;

Matches 106; Conservative .33; Mismatches 43; Indels 1; Gaps 1

QY 2 NAPRWVSLMVLVAIGTAVTAANPQVVRISQKGLDVASQGTAAQKELKRIKIPDYS 61

DB 7 NVRKSAELLALAIIGTALTAAPDPGFVAMISQKGLDFACQGVVELQELQAISSVPDFSG 66

QY 62 SFKIKHLGKHGHSFFYSMDIRFQIPSSQISWPNVGLKFSISNANIKISGKWKAQKRFLK 121

DB 67 VFKIKHLGKHGHSFFYSMAVDGFHIPNPKIEMLPDGLRVFIDKASIKINGKWSRKNFLK 126

QY 122 MSGNFDLSIEGMSISADILKLGSNPTSGKPTTICSSCSHNSVHVHISKSKVGMILQLFPH 181

DB 127 ASGNFQLSIOGVSIIADILGSD-SSGHITTCNSCDSHDSVHIKISGMLGWLIRLPH 185

QY 182 KKI 184

DB 186 RKI 188

RESULT 7

Q8BSF3

ID Q8BSF3 PRELIMINARY; PRT; 486 AA.

AC Q8BSF3;

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Mus musculus adult male epididymis cDNA, RIKEN full-length enriched library, clone:9230105K17 product:weakly similar to

DE bactericidal/permeability-increasing protein.

DE Name=9230105K17(rik).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

Best Local Similarity 57.9%; Pred. No. 1.le-40;
Matches 106; Conservative 33; Mismatches 43; Indels 1; Gaps 1;

QY 2 NAPRWLMVLVAIGTAVTAANVGVVVRISQGLDYASQOGTAALQKELKRIKIPDYS 61
Db | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
7 NVKWSALLLAIGTALTATDPGFVAMISQKGLDFACQGVVLEQLQELQALISVDFSG 66

QY 62 SFKIKHLGKHGHSFYSDIRFOLPSSQISQWPNVGLKFSISNANIKISGKWAQKFLX 121
Db | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
67 VFKIKHLGKGSYFYSNAVDGPHIPNKIEMLPSDLGRVFIKQASIKINGKWSRKNFLK 126

QY 122 MSGNFDLSIGMSADLKLGSNPTSGKPRITTCSSCSHSHSVHSHKSKVGMWLQLFH 181
Db | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
127 AGNFELISQGVISTDLILGSD-SSGHITTCNSCDSHDSVHIKISGSMGLWLRFLH 185

QY 182 KKI 184
Db |||

186 RKI 188

RESULT 8
Q9GK40 PRELIMINARY; PRT; 178 AA.
AC Q9GK40;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Bactericidal/permeability-increasing protein (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RA Xu J., Wang H.;
RP Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF322586; AAG42842.1; -.
DR HSP; P17213; 1BP1.
DR GO; GO:0008289; F:lipid binding; IEA.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP; 1.
DR SMART; SM00328; BPI1; 1.
FT NON_TER 1
FT NON_TER 178
SQ SEQUENCE 178 AA; 19693 MW; 867D7C6CA14B3A75 CRC64;

Query Match 55.0%; Score 518.5; DB 2; Length 178;
Best Local Similarity 62.5%; Pred. No. 5.5e-38;
Matches 95; Conservative 29; Mismatches 27; Indels 1; Gaps 1;

QY 33 QKGLDYASQOGTAALQKELKRIKIPDYSDFSKIKHLGKHGHSFYSDIRFOLPSSQISM 92
Db | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
1 QKGLDYACQGVAVLQKELKIRIPDVSGKFKLPFGKGHNFHSLVRSFQLPQIRL 60

QY 93 VPNVGLKFSISNANIKISGKWAQKFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTI 152
Db | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
61 QPNVGLRVISNANVRIGRWKARKGFIKVRGKFDLSVEGVSISADLKLGSPASGRATV 120

QY 153 TCSSCSHSHSVHSHKSKVGMWLQLFHKKI 184
Db | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
121 TCSSCSNINRRLRVSGILGWLKLFHKKI 151

RESULT 9
BPI_RABIT STANDARD; PRT; 445 AA.
AC Q28739;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Bactericidal permeability-increasing protein (BPI) (Fragment).
GN Name=BPI;
OS Oryctolagus cuniculus (Rabbit).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RA SEQUENCE FROM N.A.
RC STRAIN=New Zealand white; TISSUE=Bone marrow;
RA Weiss J., Weinrauch Y., Levy O., Flynn S.;
Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RL FUNCTION: The cytotoxic action of BPI is limited to many species
CC of gram-negative bacteria; this specificity may be explained by a
CC strong affinity of the very basic N-terminal half for the
CC Gram-negative charged lipopolysaccharides that are unique to the
CC Gram-negative bacterial outer envelope (By similarity).
CC -SUBCELLULAR LOCATION: Membrane-associated in polymorphonuclear
CC Leukocytes (PMN) granules (By similarity).
CC -TISSUE SPECIFICITY: Restricted to cells of the myeloid series (By
CC similarity).
CC -DOMAIN: The N-terminal region may be exposed to the interior of
CC the granule, whereas the C-terminal portion may be embedded in the
CC membrane. During phagocytosis and degradation, proteases may be
CC released and activated and cleave BPI at the junction of the N-
CC and C-terminal portions of the molecule, providing controlled
CC release of the N-terminal antibacterial fragment when bacteria are
CC ingested (By similarity).
CC -SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
CC family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@lsb-sib.ch).
CC
CC EMBL; U61270; AAB03812.1; -.
DR HSP; P17213; 1BP1.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP; 1.
DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR SMART; SM00328; BPI1; 1.
DR SMART; SM00329; BPI2; 1.
DR PROSITE; PS00400; LBP_BPI_CETP; PARTIAL.
KW Antibiotic; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 1
FT SITE 198 203 Cleavage sites for elastase (Potential).
FT TRANSMEM 327 347 Potential.
FT CARBOHYD 352 352 N-linked (GLCNAC...) (Potential).
SQ SEQUENCE 445 AA; 48837 MW; 209AE0894FEDACFC CRC64;

Query Match 53.7%; Score 506.5; DB 1; Length 445;
Best Local Similarity 62.5%; Pred. No. 1.8e-36;
Matches 95; Conservative 26; Mismatches 30; Indels 1; Gaps 1;

QY 33 QKGLDYASQOGTAALQKELKRIKIPDYSDFSKIKHLGKHGHSFYSDIRFOLPSSQISM 92
Db | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
1 QKGLDYACQGVAVLQKELKIRIPDVSGKFKLPFGKGHNFHSLVRSFQLPQIRL 60

QY 93 VPNVGLKFSISNANIKISGKWAQKFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTI 152
Db | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
61 QPNVGLRVISNANVRIGRWKARKGFIKVRGKFDLSVEGVSISADLKLGSPASGRATV 120

QY 153 TCSSCSHSHSVHSHKSKVGMWLQLFHKKI 184
Db | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
121 TCSSCSNINRRLRVSGILGWLKLFHKKI 151

RESULT 10
LBP_MOUSE STANDARD; PRT; 481 AA.
ID LBP_MOUSE
AC Q61805; Q99KA0;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

```



05-JUL-2004 (Rel. 44, Last annotation update)  
Lipopolysaccharide-binding protein precursor (LBP).  
Name=Lbp;  
Mus musculus (Mouse).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
[1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RX MEDLINE=97289150; PubMed=9144073;  
RA Lengacher S., Jongeneel C.V., le Roy D., Lee J.D., Kravchenko V.,  
RA Ulevitch R.J., Glauser M.P., Heumann D.;  
RT "Reactivity of murine and human recombinant LPS-binding protein (LBP)  
RT within LPS and Gram-negative bacteria.";  
RL J. Inflamm. 47:165-172(1995).  
RN [2]  
SEQUENCE FROM N.A.  
RP MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Wozniak K.C., Green E.D., Dickson M.C.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting J., Touchman J.W., Green E.D., Dickson M.C.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Gough G.G.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -|- FUNCTION: Binds to the lipid moiety of bacterial  
CC lipopolysaccharides (LPS), a glycolipid present in the outer  
CC membrane of all Gram-negative bacteria. The LBP/LPS complex seems  
CC to interact with the CD14 receptor.  
CC -|- SUBCELLULAR LOCATION: Secreted.  
CC -|- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP  
CC family.  
-----  
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
CC EMBL; X99347; CAA67727.1; -;  
CC EMBL; BC004795; AAH04795.1; -;  
CC HSP; P17213; LEWP  
CC MGD; MGI:1098776; Lbp.  
CC GO; GO:0001530; Filippopolysaccharide binding; IDA.  
CC InterPro; IPR001124; LBP\_BPI\_CETP.  
CC Pfam; PF01273; LBP\_BPI\_CETP; 1.  
CC Pfam; PF02886; LBP\_BPI\_CETP\_C; 1.  
CC SMART; SM00328; BPI1; 1.  
CC SMART; SM00329; BPI2; 1.  
CC PROSITE; PS00400; LBP\_BPI\_CETP; 1.  
CC Antitoxic; Glycoprotein; Lipid transport; Signal; Transmembrane.  
CC SIGNAL 1 24 Potential.  
FT CHAIN 25 481 Lipopolysaccharide-binding protein.  
FT CARBOHYD 300 300 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 355 355 N-linked (GlcNAc...) (Potential).  
FT CONFLICT 25 25 C -> G (in Ref. 2).  
FT CONFLICT 51 51 K -> Q (in Ref. 2).

FT CONFLICT 102 102 R -> S (in Ref. 2).  
FT CONFLICT 280 280 A -> S (in Ref. 2).  
FT CONFLICT 310 310 H -> P (in Ref. 2).  
FT CONFLICT 313 313 G -> S (in Ref. 2).  
FT CONFLICT 341 341 R -> G (in Ref. 2).  
FT CONFLICT 382 382 S -> G (in Ref. 2).  
FT CONFLICT 395 396 TR -> NS (in Ref. 2).  
FT CONFLICT 418 418 I -> M (in Ref. 2).  
SQ SEQUENCE 481 AA; 53312 MW; 34EA9C066C9AB678 CRC64;  
  
Query Match 47.5%; Score 448; DB 1; Length 481;  
Best Local Similarity 47.0%; Pred. No. 3e-31;  
Matches 85; Conservative 43; Mismatches 51; Indels 2; Gaps 2;  
  
Qy 4 PRWVSLMVLVAIGPAAVNVGVVRSQKGLDYASQOQTAALQKELKRIKIPDYSDSP 63  
Db 7 PLLSTLLGLLFLSIQGTGCVNPGVARITDKGLAYAAKEGLVALKRELYKITLPDFSGDF 66  
  
Qy 64 KIKHLGCHYFSYMDIREQLPSSQISMPNVNCLKFSISNANIKISKWKAKQKFLKMS 123  
Db 67 KIKAVGRGOVEFHSLQNCLEGRSSKLLPQOGLRLAISDSSIGVRKWKVRKSLKLH 126  
  
Qy 124 GNPLDSTEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKSKVGLIQLFHKK 183  
Db 127 GSFLLDKVGTISVDLLGLGMDP-SGRPTVSAGSSRICLDLVHIS-GNVGLNLNLFHQ 184  
  
Qy 184 I 184  
Db 185 I 185  
  
RESULT 11  
Q8TCF0 PRELIMINARY; PRT; 477 AA.  
ID Q8TCF0  
AC Q8TCF0; 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE LBP protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
EX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Wozniak K.C., Green E.D., Dickson M.C.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting J., Touchman J.W., Green E.D., Dickson M.C.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Liver;  
RC Strausberg R.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC022256; AAH22256.1; -.



[illegible]

05-JUL-2004 (Rel. 44, Last annotation update)  
DE Lipopolysaccharide-binding protein precursor (LBP).  
GN Name=Lbp;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
RX MEDLINE=94292804; PubMed=8021509;  
SU G.L., Frieswick P.D., Geller D.A., Wang Q., Shapiro R.A., Wan Y.H.,  
RA Billiar T.R., Tweardy D.J., Simmons R.L., Wang S.C.;  
RT "Molecular cloning, characterization, and tissue distribution of rat  
lipopolysaccharide binding protein. Evidence for extrahepatic  
expression.";  
RL J. Immunol. 153:743-752 (1994).  
CC -I- FUNCTION: Binds to the lipid moiety of bacterial  
lipopolysaccharides (LPS), a glycolipid present in the outer  
membrane of all Gram-negative bacteria. The LBP/LPS complex seems  
to interact with the CD14 receptor.  
CC -I- SUBCELLULAR LOCATION: Secreted.  
CC -I- SIMILARITY: Belongs to the BPI/LBP/Pilunc superfamily. BPI/LBP

---

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ebi.ac.uk/termsandconditions or send an email to license@ebi.ac.uk).

---

EMBL; L32132; AAA21835.1; -.  
PIR; I56246; I56246.  
HSPG; PL7213; LEWF.  
DR RGB; GI865; Lbp.  
DR InterPro; IPRO01124; LBP\_BPI\_CETP.  
DR Pfam; PF01273; LBP\_BPI\_CETP\_1.  
DR Pfam; PF02886; LBP\_BPI\_CETP\_C\_1.  
DR SMART; SM00328; BPI1; 1.  
DR SMART; SM00329; BP12; 1.  
DR PROSITE; PS00400; LBP\_BPI\_CETP; 1.  
KW Antibiotic; Glycoprotein; Lipid transport; Signal; Transmembrane.

---

SIGNAL 1 25 Potential.  
FT CHAIN 26 481 Lipopolysaccharide-binding protein.  
FT CARBOHYD 300 300 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 355 355 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 481 AA; 53600 MW; 23E67CB9C97D2FC CRC64;

---

Query Match 45.4%; Score 428; DB 1; Length 481;  
Best Local Similarity 44.2%; Pred. No. 1.8e-29;  
Matches 80; Conservative 45; Mismatches 54; Indels 2; Gaps 2

---

QY 4 PRWVSLMVLVAGTAATVAANVPVVVRISQGGLDYASOQTAALOKELKRIPYSDSF 63  
DB :|::|||::|::|::|::|::|::|::|::|::|::|::|::|:  
7 PLLPTLLGLLSLPRTGGVNPAVMVVRTDKGLEYYAKEGLSLQLRELYKITLPDFSGDF 66  
QY 64 KIKHLKGCHVSFYNDIREFOLPSSQSMTNVNVLKFSISNNAIKISGWKAOKRFKLWS 123  
DB 67 KIKAVGRGYEFHSLEIQSCQLRGSSLKPPLPGRLSLSIDSSTSVRKWKVRSFKVLH 126  
QY 124 GNFDLSIEGMNISADLKLGNSPTSGKPTITCSGCSSHINSVHVHTSKSVGVWLIIOLFHKK 183  
DB 127 GSFLDDVKSVTVISVDLLIGVDP-SERPVTVASGSNRIRDLELHSV-GNVGWLLNLFHQQ 184  
QY :184 i184  
DB 185 i 185

---

RESULT 14  
Q6GLX0





**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2005, 11:22:43 ; Search time 171.285 Seconds  
(without alignments)  
1455.954 Million cell updates/sec

Title: US-10-629-516-2  
Perfect score: 2507  
Sequence: 1 MRENARGPCNAPRWVSLMV.....NVVLQPHONFLFGADVVK 487

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2500	99.7	487	2	Q81W58
2	2486	99.2	483	1	BPI HUMAN
3	1627.5	64.9	482	1	BPI BOVIN
4	1507.5	60.1	445	1	BPI RABIT
5	1415.5	56.5	482	2	Q6AXU0
6	1361	54.3	483	2	Q67E05
7	1349.5	53.8	486	2	Q8BSF3
8	1145.5	45.7	476	2	Q6GLX0
9	1088	43.4	481	1	LBP HUMAN
10	1062	42.4	477	2	Q8TGF0
11	1039	41.4	481	1	LBP RAT
12	1030	41.1	481	1	LBP MOUSE
13	985.5	39.3	482	1	LBP RABIT
14	870.5	34.7	473	2	Q8JFX3
15	867.5	34.6	473	2	Q8JFX4
16	867	34.6	473	2	Q804Q9
17	814	32.5	473	2	Q7T3Q8
18	814	32.5	473	2	Q7T3Q9
19	811	32.3	179	2	Q9GK39
20	621.5	24.8	178	2	Q9GK40
21	541	21.6	507	1	BPL2 HUMAN
22	500.5	20.0	509	1	BPL2 MOUSE
23	465	18.5	493	1	PLTP_HUMAN
24	463.5	18.5	493	1	PLTP_MOUSE
25	452.5	18.0	477	2	Q817Z9
26	450	17.9	496	2	Q8WMN7
27	434	17.3	483	2	Q661U4
28	433.5	17.3	503	2	Q8WNQ5
29	433.5	17.3	503	2	Q9S5Q0
30	425	17.0	486	2	Q6DEI0
31	386.5	15.4	515	2	Q8VYC2

32	337.5	13.5	488	2	Q9MAU5
33	336.5	13.4	488	2	Q8LAL8
34	317	12.6	1424	2	Q9LTR5
35	295	11.8	493	1	CETP HUMAN
36	287	11.4	458	2	Q6UWN3
37	283	11.3	458	2	Q6ZME0
38	282	11.2	127	2	Q9NOL9
39	282	11.2	493	1	CETP MACFA
40	278	11.1	458	1	BPI HUMAN
41	271.5	10.8	497	1	CETP RABIT
42	267.5	10.7	485	2	Q9BG59
43	261.5	10.4	470	1	LPC4 RAT
44	260.5	10.4	462	1	BPI MOUSE
45	252.5	10.1	449	1	BPL3 MOUSE

## ALIGNMENTS

RESULT 1

Q81W58 PRELIMINARY; PRT; 487 AA.

AC Q81W58; DT 01-NAR-2003 (Tremblrel. 23, Created)

DT 01-NAR-2003 (Tremblrel. 23, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Bactericidal/permeability-increasing protein, .

GN Name=BPI;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1] SEQUENCE FROM N.A.

RC TISSUE=Blood;

RX MEDLINE=223888257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2] SEQUENCE FROM N.A.

RP TISSUE=Blood;

RC Strausberg R.;

RA Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

RL EMBL; BC040955; AAH40955.1; -.

DR HSP; P17213; 1EWP.

DR GO; GO:0008289; F.lipid binding; IEA.

DR InterPro; IPR01124; LBP\_BPI\_CETP.

DR Pfam; PF01273; LBP\_BPI\_CETP; 1.

DR Pfam; PF02886; LBP\_BPI\_CETP\_C; 1.

DR SMART; SM00328; BPI1; 1.

DR SMART; SM00329; BPI2; 1.

DR PROSITE; PS00400; LBP\_BPI\_CETP; 1.

SQ SEQUENCE 487 AA; 53860 MW; FE709D9317E5206D CRC64;

Query Match 99.7%; Score 2500; DB 2; Length 487;

Best Local Similarity		99.6%;	Pred. No. 2.2e-181;				
Matches		485;	Conservative	1;	Mismatches	1;	Indels



This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

```

-----
CC EMBL; J04739; AAA51841.1; ALT INIT.
CC EMBL; AF322588; AAG42844.1; -
CC EMBL; AL359555; CAC13043.1; -
CC EMBL; AL499625; CAC27350.1; -
CC EMBL; AL391692; CAC10453.1; -
CC PDB; 1BP1; X-ray; @=28-483.
CC PDB; 1EWF; X-ray; A=28-483.
CC Genew; HGNC:1095; BPI.
CC MIM; 109195; -
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC InterPro; IPR001124; LBP_BPI_CETP.
CC Pfam; PF01273; LBP_BPI_CETP; 1.
CC Pfam; PF02886; LBP_BPI_CETP_C; 1.
CC SMART; SM00328; BPI1; 1.
CC SMART; SM00329; BPI2; 1.
CC PROSITE; PS00400; LBP_BPI_CETP; 1.
CC 3D-structure; Antibiotic; Direct protein sequencing; Glycoprotein;
CC Polymorphism; Signal; Transmembrane.
KW SIGNAL 1 27
KW CHAIN 28 483
FT SITE 236 241 Bactericidal permeability-increasing
FT TRANSMEM 365 385 Protein.
FT VARIANT 12 12 Cleavage sites for elastase (Potential).
FT VARIANT 192 192 V -> A (in dbSNP:1341023).
FT VARIANT 212 212 A -> V (in dbSNP:5743509).
FT VARIANT 351 351 K -> E (in dbSNP:4358188).
FT CONFLICT 371 371 P -> S (in Ref. 3).
FT CONFLICT 400 400 F -> L (in Ref. 2).
FT CONFLICT 407 407 N -> D (in Ref. 3).
FT STRAND 32 37 K -> R (in Ref. 3).
FT HELIX 38 56
FT TURN 57 58
FT STRAND 64 67
FT STRAND 77 89
FT STRAND 93 98
FT TURN 99 101
FT STRAND 102 122
FT TURN 123 124
FT STRAND 125 149
FT TURN 150 153
FT STRAND 154 165
FT STRAND 168 172
FT HELIX 176 178
FT TURN 179 188
FT TURN 189 189
FT HELIX 190 211
FT TURN 212 212
FT TURN 213 217
FT TURN 218 219
FT STRAND 223 225
FT STRAND 231 233
FT STRAND 236 236
FT STRAND 241 242
FT STRAND 246 251
FT STRAND 254 256
FT STRAND 281 286
FT HELIX 287 299
FT TURN 300 301
FT STRAND 304 308
FT HELIX 309 311
FT TURN 314 315

```

```

FT STRAND 321 321
FT HELIX 322 326
FT TURN 327 328
FT HELIX 332 335
FT TURN 337 338
FT STRAND 340 346
FT STRAND 352 356
FT TURN 357 358
FT STRAND 359 363
FT STRAND 365 373
FT TURN 375 376
FT STRAND 379 388
FT STRAND 391 397
FT STRAND 401 408
FT STRAND 412 418
FT HELIX 425 428
FT HELIX 429 439
FT TURN 440 440
FT HELIX 441 450
FT STRAND 452 453
FT TURN 458 459
FT STRAND 460 470
FT TURN 471 472

Query Match 99.2%; Score 2486; DB 1; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.5e-180;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 MARGPCNAPRWLSLMLVLAIGTAVTAANPVGVVVRISQKGLDYASQQGTAALQKELKRIK 64
DB 1 MARGPCNAPRWLSLMLVLAIGTAVTAANPVGVVVRISQKGLDYASQQGTAALQKELKRIK 60
QY 65 IPDYSDFSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKA 124
DB 61 IPDYSDFSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKA 120
QY 125 QKRFKMSGNFPLDSIEGMSISADLKGSNPTSGKPTITCSCSSSHINSVHVHISKSKYGM 184
DB 121 QKRFKMSGNFPLDSIEGMSISADLKGSNPTSGKPTITCSCSSSHINSVHVHISKSKYGM 180
QY 185 LIQLFHKKIESALRNKNMSQVCEKVTNSVSSKLQPYFOTLPVMTKIDS VAGINYLGLVAPP 244
DB 181 LIQLFHKKIESALRNKNMSQVCEKVTNSVSSKLQPYFOTLPVMTKIDS VAGINYLGLVAPP 240
QY 245 ATTAETLDVQKGEFYSENHNPPFPAPPVMEFPAADHDMVYLGISDYFFNTAGLYQEA 304
DB 241 ATTAETLDVQKGEFYSENHNPPFPAPPVMEFPAADHDMVYLGISDYFFNTAGLYQEA 300
QY 305 GVLKMTLRDDMI PKESKFRLLTKFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQPTGL 364
DB 301 GVLKMTLRDDMI PKESKFRLLTKFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQPTGL 360
QY 365 TFYPADVQVQAFVLPNSLSLFLIGHMTTCSMEVSASNRILVGLKLDRLLELKHSNI 424
DB 361 TFYPADVQVQAFVLPNSLSLFLIGHMTTCSMEVSASNRILVGLKLDRLLELKHSNI 420
QY 425 GPPFVELLDIMNTYIPILVLPVNEKIQKGFPLTPARVOLYNNVLPHQNFLLFGADV 484
DB 421 GPPFVELLDIMNTYIPILVLPVNEKIQKGFPLTPARVOLYNNVLPHQNFLLFGADV 480
QY 485 VYK 487
DB 481 VYK 483

RESULT 3
BPI_BOVIN
ID BPI_BOVIN STANDARD; PRT; 482 AA.
AC P17453;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Bactericidal permeability-increasing protein precursor (BPI).

```

GN Name=BPI;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RA MEDLINE=90272418; PubMed=2349103;  
RX Leong S.R., Camerato T.;  
RT "Nucleotide sequence of the bovine bactericidal permeability  
RL Nucleic Acids Res. 18:3052-3052(1990).  
CC -I- FUNCTION: The cytotoxic action of BPI is limited to many species  
CC of Gram-negative bacteria; this specificity may be explained by a  
CC strong affinity of the very basic N-terminal half for the  
CC negatively charged lipopolysaccharides that are unique to the  
CC Gram-negative bacterial outer envelope.  
CC -I- SUBCELLULAR LOCATION: Membrane-associated in polymorphonuclear  
CC Leukocytes (PMN) granules (By similarity).  
CC -I- TISSUE SPECIFICITY: Restricted to cells of the myeloid series (By  
CC similarity).  
CC -I- DOMAIN: The N-terminal region may be exposed to the interior of  
CC the granule, whereas the C-terminal portion may be embedded in the  
CC membrane. During phagocytosis and degranulation, proteases may be  
CC released and activated and cleave BPI at the junction of the N-  
CC and C-terminal portions of the molecule, providing controlled  
CC release of the N-terminal antibacterial fragment when bacteria are  
CC ingested (By similarity).  
CC -I- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP  
CC family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; X52563; CAA36797.1; -  
CC PIR; S10180; S10180.  
CC HSP; P17213; IEF.  
CC InterPro; IPR001124; LBP\_BPI\_CETP.  
CC Pfam; PF01273; LBP\_BPI\_CETP; 1.  
CC Pfam; PF02886; LBP\_BPI\_CETP\_C; 1.  
CC SMART; SM00328; BPI1; 1.  
CC SMART; SM00329; BPI2; 1.  
CC PROSITE; PS00400; LBP\_BPI\_CETP; 1.  
KW Antibiotic; Glycoprotein; Membrane; Signal.  
FT SIGNAL 1 26  
FT CHAIN 27 482  
FT  
FT SITE 235 240 Bactericidal permeability-increasing  
FT Cleavage sites for elastase (Potential).  
FT CARBOHYD 62 62 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 303 303 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 375 375 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 389 389 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 482 AA; 53432 MW; DD7D59AE785BC42D CRC64;  
Query Match 64.9%; Score 1627.5; DB 1; Length 482;  
Best Local Similarity 63.5%; Pred. No. 4.4e-115;  
Matches 306; Conservative 81; Mismatches 94; Indels 1; Gaps 1;  
  
QY 5 MARGPCNAPWSIMVLVAITGTAATAVNVGVVRISQKGLDYASQGTAALOKELKRIK 64  
DB 1 MARGPDTARWATLVLLVLAIGTAVT-TTNPGIVARITQKGLDYACQGVLTLOKELEKIT 59  
QY 65 IPDYSDSFKIKHLKGHSYFSMDIREFQLPSSQISMPVNVGKLFSTSNANIKISGKWA 124  
DB 60 IPNFSGNFKIKYLGKGYSFSSVMVIOGFNLPNSQIRPLPKGLDLSIRDSIKIRGKWA 119

QY 125 QKFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHISKVKVG 184  
DB 120 RKNFIKLGNGFDLSVEGISILAGNLGYDPASGHSTVITCSSSGGINTVRIHISGSLGW 179  
QY 185 LIQLFHKKIESALRNKNQSQVCEKVTNSVSSKLQPYFQTLPVNMTKIDSVAGINYLVA 244  
DB 180 LIQLFRKRIESLLQKSMTRKICEVTVSTVSSKLQPYFQTLPVTTKLDKAGVDVSLV 239  
QY 245 ATTAETLDVOMKGEFFYSVSENNHPPPPAPVMEFPAADHDMVYLGLSDYFNTAGLV 304  
DB 240 RATANNLDWLLKGEFFSLAHRSPPPAPPALAPPSSDHRMVLGISEYFFENTAGVY 299  
QY 305 GVLKMTLRDMDPKESKFRLLTKFFCTFLPEVAKKFPNMKIOIHVSASTPHLSVOP 364  
DB 300 GALLNLTLDMDPKESKFRLLTKFFGILIPQVAKMFPDMQMFIVASLPPKLTMKP 359  
QY 365 TFPYADVQAFVLPNSSLASFLIGMHTTGSMEVSAESNRLVGELKLDRLLELKH 424  
DB 360 DLIFVLDTQAFALLPNSSLDPLFLEMLNLSVVGAKSDRLIGELRLDKLLELKH 419  
QY 425 GPFVVELLDQIMNYIVPIVLPRVNEKLOKGPPLPTPARVOLYNNVLQPHNQNF 484  
DB 420 GPFVESLQSVINYVMPTIVLPVINKLOKGFPLPLPAYIEFLNLTLPQYQDFLFG 479  
QY 485 VY 486  
DB 480 QY 481  
  
RESULT 4  
BPI\_RABIT  
ID BPI\_RABIT STANDARD; PRT; 445 AA.  
AC Q28739;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Bactericidal permeability-increasing protein (BPI) (Fragment).  
GN Name=BPI;  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=New Zealand white; TISSUE=Bone marrow;  
RA Weiss J., Weinrauch Y., Levy O., Flynn S.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
CC -I- FUNCTION: The cytotoxic action of BPI is limited to many species  
CC of Gram-negative bacteria; this specificity may be explained by a  
CC strong affinity of the very basic N-terminal half for the  
CC negatively charged lipopolysaccharides that are unique to the  
CC Gram-negative bacterial outer envelope (By similarity).  
CC -I- SUBCELLULAR LOCATION: Membrane-associated in polymorphonuclear  
CC Leukocytes (PMN) granules (By similarity).  
CC -I- TISSUE SPECIFICITY: Restricted to cells of the myeloid series (By  
CC similarity).  
CC -I- DOMAIN: The N-terminal region may be exposed to the interior of  
CC the granule, whereas the C-terminal portion may be embedded in the  
CC membrane. During phagocytosis and degranulation, proteases may be  
CC released and activated and cleave BPI at the junction of the N-  
CC and C-terminal portions of the molecule, providing controlled  
CC release of the N-terminal antibacterial fragment when bacteria are  
CC ingested (By similarity).  
CC -I- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP  
CC family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; X52563; CAA36797.1; -  
CC PIR; S10180; S10180.  
CC HSP; P17213; IEF.  
CC InterPro; IPR001124; LBP\_BPI\_CETP.  
CC Pfam; PF01273; LBP\_BPI\_CETP; 1.  
CC Pfam; PF02886; LBP\_BPI\_CETP\_C; 1.  
CC SMART; SM00328; BPI1; 1.  
CC SMART; SM00329; BPI2; 1.  
CC PROSITE; PS00400; LBP\_BPI\_CETP; 1.  
KW Antibiotic; Glycoprotein; Membrane; Signal.  
FT SIGNAL 1 26  
FT CHAIN 27 482  
FT  
FT SITE 235 240 Bactericidal permeability-increasing  
FT Cleavage sites for elastase (Potential).  
FT CARBOHYD 62 62 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 303 303 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 375 375 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 389 389 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 482 AA; 53432 MW; DD7D59AE785BC42D CRC64;  
Query Match 64.9%; Score 1627.5; DB 1; Length 482;  
Best Local Similarity 63.5%; Pred. No. 4.4e-115;  
Matches 306; Conservative 81; Mismatches 94; Indels 1; Gaps 1;  
  
QY 5 MARGPCNAPWSIMVLVAITGTAATAVNVGVVRISQKGLDYASQGTAALOKELKRIK 64  
DB 1 MARGPDTARWATLVLLVLAIGTAVT-TTNPGIVARITQKGLDYACQGVLTLOKELEKIT 59  
QY 65 IPDYSDSFKIKHLKGHSYFSMDIREFQLPSSQISMPVNVGKLFSTSNANIKISGKWA 124  
DB 60 IPNFSGNFKIKYLGKGYSFSSVMVIOGFNLPNSQIRPLPKGLDLSIRDSIKIRGKWA 119

or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

```
CC -----
CC EMBL; U61270; AAB03812.1; -.
DR HSSP; P17213; LBPI.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP; 1.
DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR SMART; SM00328; BPI1; 1.
DR SMART; SM00329; BPI2; 1.
DR PROSITE; PS00400; LBP_BPI_CETP; PARTIAL.
KW Antibiotic; Glycoprotein; Transmembrane.
FT SITE 198 203 Cleavage sites for elastase (Potential).
FT TRANSMEM 327 347 Potential.
FT CARBOHYD 352 352 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 445 AA; 48837 MW; 209AE0894FEDACFC CRC64;
```

```
Query Match 60.1%; Score 1507.5; DB 1; Length 445;
Best Local Similarity 63.0%; Pred. No. 5.2e-106;
Matches 279; Conservative 80; Mismatches 83; Indels 1; Gaps 1;

QY 42 QKGLDYASQGTAAQKELKRIKIPDYSDFKIKHLGKHGHSFYSDMIREFOLPSSQISM 101
DB 1 QKGLDYACQGVAVLQKELEKIRIPDVSGKFKLRPFKRGHYNFHSLVRSFQLPAPQIRL 60

QY 102 VENVGLKFSISNANIKISGKKAQKRFKMGNFOLSIIEGMSISADLKLGSNPTSGKPTI 161
DB 61 QNVGLRVISINAVNRIGRWARKGFIKVRGKFDLSVEGVSISADLKLGSVPASGRATV 120

QY 162 TCSSCSSHNSVHVHISKVGWLIQFHKKIESALRNQNSQVCEKVTNSVSSKLQPYF 221
DB 121 TCSSCSSHNSNRRARLSQASGCGWL-KLFHKRIESSLRNTMNSKIQVLTSVSSKLQPV 179

QY 222 QTLPMWTKIDSAGINYGAVAPATTAETLDVQMGGEFYSENNHNPFPAPVMEFPAAH 281
DB 180 ETLPLKRLDSVAGIDYSLVAPPRATADSLDQMGGEFYFNVARPPPPMPMAIPSLH 239

QY 282 DRMWYGLSDYFENTAGLVYQAGVLMKTRDDMIPKESKFRLLTKFFGTFTLPEVAKKPP 341
DB 240 DRMWYLAISDYLFENTAAVYQAGAFGLTRDDMIPKESKRLTKFLGKALPQVAKMPP 299

QY 342 NMKIQHVSASTPPHLSVQPTGLTFYPADVQAFVLPNSSLASLFLIGHMTTGSMEVSA 401
DB 300 NMNVQLTSLVSSPPHLLTRPTGIALTAADVQAFVLPNSSLASLFLGLKLNTSAKIGT 359

QY 402 ESNRLVGELKLRLLLELKHSGNIGPPVELLDIMNYIVPILVLRVNEKLGKGEPLTP 461
DB 360 KADKLVGELTLGRLLLELKHSGNIGSFPVQLQALMDYVLSAVVLPKVNKLGQGLPMP 419

QY 462 ARVOLNVVLPQHONFLFGADV 484
DB 420 RKVQLYDLVLQPHQDFLLGNV 442
```

```
RESULT 5
Q6AXU0 PRELIMINARY; PRT; 482 AA.
ID Q6AXU0
AC Q6AXU0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Bactericidal/permeability-increasing protein.
GN Name=Bpi;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
```

```
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Caavaant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Director MGC Project;
RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
EMBL; BC079318; AAB79318.1; -.
GO; GO:0008289; F:lipid binding; IEA.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP; 1.
DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR SMART; SM00328; BPI1; 1.
DR SMART; SM00329; BPI2; 1.
SQ SEQUENCE 482 AA; 53751 MW; 269591C4C2F5A6D1 CRC64;
```

```
Query Match 56.5%; Score 1415.5; DB 2; Length 482;
Best Local Similarity 55.8%; Pred. No. 5.7e-99;
Matches 268; Conservative 89; Mismatches 122; Indels 1; Gaps 1;

QY 5 MARGPCNAPRWVSLMVLVAIGTAVTAANNPGVVVIRISOKGLDYASQGTAAQKELKRIK 64
DB 1 MARGPCNVRKSSSLALLAIVGTALTAAATDPGFVARISOKGLDFVQCESMVELQKELLALS 60

QY 65 IDPYSDSKIKHLGKHGHSFYSDMIREFOLPSSQISMPNVGLKFSISNANIKISGKKA 124
DB 61 IDPDSGDFKIRHLGKHGTYEFYSMAVEGHIPDPQIKLPSDGLQISITSASIKISRWKY 120

QY 125 QKRFLKMGNFOLSIIEGMSISADLKLGSNPTSGKPTITCSSCSSHNSVHVHISKVGW 184
DB 121 RKNILKASGNFOLSIQGVSLIADLILGNDP-SGRITITCTCDSHNSVRIKVGSGMLGW 179

QY 185 LIQLFHKKIESALRNQNSQVCEKVTNSVSSKLQPYFQTLPMVKIDSVAGINYLAVPP 244
DB 180 LIQLFHRKIETSLKTIYKKICKIVRNSVSAKLQPVKTLPPVAVKVDITSDISLLAPP 239

QY 245 ATTAETLDVQMGGEFYSENNHNPFPAPVMEFPAADHDMVYLGUSDYFENTAGLVYQEA 304
DB 240 MTTDKFLEGLRGGEFFWRGHGFPFAPVPEVMNLPNNNYMVCMSISDYFFNTAEFAYES 299

QY 305 GVLKMTLRDDMIPKESKFRLLTKFFGTFTLPEVAKKFPNNMKIQIHVSASTPPHLSVQPTGL 364
DB 300 ETLKITLRDQLAKADARYHLNTDFLTKTLPEVAKKFPNSMGLQLLISAPLFAHLNIQPSGL 359

QY 365 TFYPADVQAFVLPNSSLASLFLIGHMTTGSMEVSAESNRLVGELKLRLLLELKHSGNI 424
DB 360 SLSPNLETRAFVVLNSSLIPFLFLGKMTNASLEVNAMKNRLIGEMKGLRLLLELQSNF 419

QY 425 GFFPVELLDIMNYIVPILVLRVNEKLGKGEPLTPPARVOLNVVLPQHONFLFGADV 484
DB 420 GSKFVELLEDVINYLMSTMVLPKINEKLRGRGFPPLPAGIQLINSILYSQNFLLLEADL 479
```

```
RESULT 6
Q67E05 PRELIMINARY; PRT; 483 AA.
ID Q67E05
AC Q67E05;
```



```
SQ SEQUENCE 486 AA; 54351 MW; 908F627EA5496D62 CRC64;
Query Match 53.8%; Score 1349.5; DB 2; Length 486;
Best Local Similarity 53.7%; Pred. No. 6e-94;
Matches 260; Conservative 90; Mismatches 129; Indels 5; Gaps 3;
QY 5 MARGPCNAPRWVSLMVLVAIGTAVTAANPGVVRISQGLDYASQOQTAAALQKELKRIK 64
DB 1 MTWAPDNVRKWSALLLAIIGTALTAAATDQGFVAMISQGLDFACQOQWELQKLOAIS 60
QY 65 IPDYSDSFKIKHLGKHGHSFYSDIREFOLPSSQISMPVNVGLKFSISNANIKISGKWK 124
DB 61 VPDESGVFVKIKHLGKHGHSYEFYSMDVGFHINPKIEMLPDGLRVFIKDSIKINGKWS 120
QY 125 QKRFLKMGNFDSLTEGMSISADLKGSNPTSGKPTITCSCSSHINSVHVHISKSKVG 184
DB 121 RKNFLKAGNFELSIOGVSISTDLILGSD-SSGHITTCNSCDSHIDSVHIKISGMLGW 179
QY 185 LIQLFHKKIESALRNKMSQVCEKVTNSVSKLQPYFOTLPVMTKIDSVAGINYLVA 244
DB 180 LIRLFHKKIESALRNKMSQVCEKVTNSVSKLQPYFOTLPVMTKIDSVAGINYLVA 239
QY 245 ATTAETLDVQMKGEFYSNHNPPFPAPVMEFPAAHDMVYLGSLDYEFNTAGLVQOE 304
DB 240 TTTNQFLGOLKGEFFWGRHDPDLPPIHPPVVRFPVNGAYMCMGSDYFENTVLA 299
QY 305 GVLKMTLRDDMI PKESKFRLLTKFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQ 364
DB 300 GTLKMVLGQLLNNGRFQNTDFLRTFLPKVAKNFPSPMGVQLLISAPVPHLSIQ 359
QY 365 TTFYPAVDVQAPVLPNSLASLFLGM---HTGSMVSAESNRNLVGLKLDRLLE 420
DB 360 SFNPKLETOAFVLPVNASLVPFLVGMVRRKTNASLEVDENRVLGEMKLSRLLE 419
QY 421 HSNIGPPVELLQDINMIVIPILVLPVNEKLOKGFPLTPARVOLYNVQLPHQNF 480
DB 420 ESKGPFVKEVLEEDVINYLVSTLVLPKINERLRGRFPLPAGIRFSHTFYQNF 479
QY 481 GADV 484
DB 480 EADL 483
```

```
RESULT 8
O6GLX0 PRELIMINARY; PRT; 476 AA.
AC O6GLX0;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE MGC84153 protein.
GN Name=MGC84153;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]_TaxID=8355;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.P., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
```

```
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC074326; AAH74326.1;
DR GO; GO:0008289; F:lipid binding; IEA.
DR InterPro; IPR005503; FliL.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF03748; FliL; 1.
DR Pfam; PF01273; LBP_BPI_CETP; 1.
DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR SMART; SM00328; BPI; 1.
DR SMART; SM00329; BPI; 1.
SQ SEQUENCE 476 AA; 52117 MW; 595F36DB5AB8B05D CRC64;
Query Match 45.7%; Score 1145.5; DB 2; Length 476;
Best Local Similarity 45.7%; Pred. No. 1.9e-78;
Matches 221; Conservative 99; Mismatches 155; Indels 9; Gaps 3;
QY 4 NMARGPCNAPRWVSLMVLVAIGTAVTAANPGVVRISQGLDYASQOQTAAALQKELKRI 63
DB 2 NIAVG-----LTFLSMAAPVGTATDGTGNGFVVRVLTQKGLDYALQEGMIVLQQLPQI 54
QY 64 KIPDYSDFKIKHLGKHGHSFYSDIREFOLPSSQISMPVNVGLKFSISNANIKISGKWK 123
DB 55 QLPDFSGTYDVLGKGVKRYRFSMTISSVQLPSYQVIVPVPDKGLKLSISGAFIQVDGRWD 114
QY 124 AQKFLKMGNFDSLTEGMSISADLKGSNPTSGKPTITCSCSSHINSVHVHISKSKVG 183
DB 115 VRYSEIHEDGSFNKVLGISISVGLIGSD-ESGRPTIAPSDCSCHISNVEVHMS-GTIG 172
QY 184 WLIIQLFHKKIESALRNKMSQVCEKVTNSVSKLQPYFOTLPVMTKIDSVAGINYLVA 243
DB 173 WLVDLFHNNVESLRSQSMENKICPEVTQSISSKLLPLLQTLPTVTTKIDQISAIDYSLTGP 232
QY 244 PATTAETLDVQMKGEFYSNHNPPFPAPVMEFPAAHDMVYLGSLDYEFNTAGLVQOE 303
DB 233 PSVMANWIDVLKGEFFDISHRTTPFPFPVMSLPPEQDLVYFAVSEYLFNTAGFVYQD 292
QY 304 AGVLKMTLRDDMI PKESKFRLLTKFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQPTG 363
DB 293 AGALVFNLTDDMI PKESSHNLNTSSFGILLISIKMYPNMLMKLISITASALAIKPGN 352
QY 364 LTFYPAVDVQAPVLPNSLASLFLIGMHTTSGSMVSAESNRNLVGLKLDRLLELKHNS 423
DB 353 LTLSPVGNIOQAVAILPNSLSLAPLFLQLNTNVLAKVAVNSGKIVGSLDKVEIQLVQSD 412
QY 424 TGPFPVELLQDINMIVIPILVLPVNEKLOKGFPLTPARVOLYNVQLPHQNFLLFGAD 483
DB 413 VGFPSVSLSTAVNYVVSATLLPRVNEILKNGYPLIEHIIQLTDFVIQTYSHYLLFGAN 472
QY 484 VVYK 487
DB 473 AHYE 476
```

```
RESULT 9
LBP_HUMAN
ID_LBP_HUMAN STANDARD; PRT; 481 AA.
AC P18428; Q43438; Q92672; Q9H403; Q9UD66;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lipopolysaccharide-binding protein precursor (LBP).
GN Name=LBP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90385281; PubMed=2402637;
RA Schumann R.R., Leong S.R., Flagg G.W., Gray P.W., Wright S.D.,
RA Mathison J.C., Tobias P.S., Ulevitch R.J.;
RT "Structure and function of lipopolysaccharide binding protein.";
RL Science 249:1429-1431(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94292492; PubMed=7517398;
RA Wilde C.G., Seilhamer J.J., McGrogan M., Ashton N., Snable J.L.,
RA Lane J.C., Leong S.R., Thornton M.B., Miller K.L., Scott R.W.;
RT "Bactericidal/permeability-increasing protein and lipopolysaccharide
RT (LPS)-binding protein. LPS binding properties and effects on LPS-
RT mediated cell activation.";
RL J. Biol. Chem. 269:17411-17416(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA Hubacek J.A., Agranidis C., Schmitz G.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=98110577; PubMed=9441745; DOI=10.1006/geno.1997.5030;
RA Kirschning C.J., Au-Young J., Lamping N., Reuter D., Pfeil D.,
RA Seilhamer J.J., Schumann R.R.;
RT "Similar organization of the lipopolysaccharide-binding protein (LBP)
RT and phospholipid transfer protein (PLTP) genes suggests a common gene
RT family of lipid-binding proteins.";
RL Genomics 46:416-425(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Long J.Y., Liu J.Q., Xue Y.N., Wang H.X.;
RT "Cloning and sequencing of human lipopolysaccharide-binding protein
RT gene.";
RL Sheng Wu Hua Xue Yu Sheng Wu Wu Li Jin Zhan 25:469-471(1998).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhali P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaealsho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McLeay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Pathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuce C.D., Smith M.T., Soderlund C., Steward C.A., Sulston J.E.,
```



```
DR Pfam; PF01273; LBP_BPI_CETP; 1.
DR SMART; PF02886; LBP_BPI_CETP_C; 1.
DR SMART; SM00328; BPI1; 1.
DR SMART; SM00329; BPI2; 1.
DR PROSITE; PS00400; LBP_BPI_CETP; 1.
KW Antibiotic; Glycoprotein; Lipid transport; Signal; Transmembrane.
FT SIGNAL 1 25
FT CHAIN 26 481
FT CARBOHYD 300 300
FT CARBOHYD 355 355
FT CARBOHYD 386 386
FT CARBOHYD 394 394
FT CARBOHYD 394 394
FT CONFLICT 6 6
FT CONFLICT 22 22
FT CONFLICT 82 82
FT CONFLICT 128 128
FT CONFLICT 154 157
FT CONFLICT 174 174
FT CONFLICT 257 257
FT CONFLICT 266 270
FT CONFLICT 369 369
FT CONFLICT 436 436
FT CONFLICT 436 436
SQ SEQUENCE 481 AA; 53349 MW; 81654B95E5E6864D0 CRC64;

Query Match 43.4%; Score 1088; DB 1; Length 481;
Best Local Similarity 44.8%; Pred. No. 4.4e-74;
Matches 210; Conservative 96; Mismatches 161; Indels 2; Gaps 2;

QY 18 LMLVVAIGTAVTAANPGVVRISOKGLDYASQOQTAAALQKELKRIKIPDYSDFKIKHL 77
DB 12 LLALLLTSTPEALGANPGVLARITDKGLQYAAQEGLLALQSELLRITLPDFTGDLRIPIHV 71

QY 78 GKGHYSFYSMDIREPOLPSSQISQIMVNVGLKFSISNANIKISGKWAQKRFKMGSGNFDL 137
DB 72 GGRGYEFHSLNIHSCHELLHSALRPVPGQGLSLISDSIRVQGRWKVRKSPFKLQSGSDV 131

QY 138 STEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHIKSKVGLWLIQFHKKIESAL 197
DB 132 SVKGISISVNLILGSE-SSGRPTVTASSCSDIADVEVDM5-GDLGWLNLNLFHNQIESKF 189

QY 198 RNKMSQVCEKVTNSVSSKLOPYFOTLPVMTKIDSVAGINYLGLVAPPATTATLTDVQMGK 257
DB 190 QKVLESRICEMTQKSVSDLOPYLQTLPTVTTEIDSFADIDSLVBPATQMLEVPMFKG 249

QY 258 EYSENHNHPPPPFAPVPMVEFPAADRMVYLGLSDYFFNTAGLVYQAGVGLKMTLDDMIP 317
DB 250 EIFHRNHRSPVTLAAVMSLPEHNKQVYFAISDVVNTASLVYHEEGLNFSITDDMIP 309

QY 318 KESKRLTTKFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQPTGLTFYPADVDQAFV 377
DB 310 PDSNIRLTTSKFRPFVPRLARLYPNMNLQSGVSPAPLNFSPGNLSVDPYMEIDAFLV 369

QY 378 LPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKDLRLLELKHGNIQPPFVELLDIMN 437
DB 370 LPSSSKPEVFRISVATNVSATLTFTNTSKITGFKPKGVKVELKSKVGLFNALLEALLN 429

QY 438 YIVPILVLRVNEKLOKGFPLTPARVQLYNNVLOPHQNLFLFGADVY 466
DB 430 YIILNTLYPKFNDKLAEGFPLLRKLVQYLDIGLQHKDFLFLGANVQY 478

RESULT 10
Q8TCF0
ID Q8TCF0 PRELIMINARY; PRT; 477 AA.
AC Q8TCF0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LBP protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```

```

[1]
SEQUENCE FROM N.A.
RN RP TISSUE=Liver;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalutz D.E., Schnerch A., Schein J.E.,
RT Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
SEQUENCE FROM N.A.
RN RP TISSUE=Liver;
RX TISSUE=Liver;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022256; AAH22256.1; -.
DR HSSP; PI7213; IEWF.
DR GO; GO:0008289; F:lipid binding; IEA.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP; 1.
DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR SMART; SM00328; BPI1; 1.
DR SMART; SM00329; BPI2; 1.
DR PROSITE; PS00400; LBP_BPI_CETP; 1.
SQ SEQUENCE 477 AA; 52933 MW; 03D5E9D55A3BA6D0 CRC64;

Query Match 42.4%; Score 1062; DB 2; Length 477;
Best Local Similarity 44.6%; Pred. No. 4.2e-72;
Matches 205; Conservative 94; Mismatches 159; Indels 2; Gaps 2;

QY 18 LMLVVAIGTAVTAANPGVVRISOKGLDYASQOQTAAALQKELKRIKIPDYSDFKIKHL 77
DB 12 LLALLLTSTPEALGANPGVLARITDKGLQYAAQEGLLALQSELLRITLPDFTGDLRIPIHV 71

QY 78 GKGHYSFYSMDIREPOLPSSQISQIMVNVGLKFSISNANIKISGKWAQKRFKMGSGNFDL 137
DB 72 GGRGYEFHSLNIHSCHELLHSALRPVPGQGLSLISDSIRVQGRWKVRKSPFKLQSGSDV 131

QY 138 STEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHIKSKVGLWLIQFHKKIESAL 197
DB 132 SVKGISISVNLILGSE-SSGRPTVTASSCSDIADVEVDM5-GDLGWLNLNLFHNQIESKF 189

QY 198 RNKMSQVCEKVTNSVSSKLOPYFOTLPVMTKIDSVAGINYLGLVAPPATTATLTDVQMGK 257
DB 190 QKVLESRICEMTQKSVSDLOPYLQTLPTVTTEIDSFADIDSLVBPATQMLEVPMFKG 249

QY 258 EYSENHNHPPPPFAPVPMVEFPAADRMVYLGLSDYFFNTAGLVYQAGVGLKMTLDDMIP 317
DB 250 EIFHRNHRSPVTLAAVMSLPEHNKQVYFAISDVVNTASLVYHEEGLNFSITDDMIP 309

QY 318 KESKRLTTKFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQPTGLTFYPADVDQAFV 377
DB 310 PDSNIRLTTSKFRPFVPRLARLYPNMNLQSGVSPAPLNFSPGNLSVDPYMEIDAFLV 369

QY 378 LPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKDLRLLELKHGNIQPPFVELLDIMN 437
DB 370 LPSSSKPEVFRISVATNVSATLTFTNTSKITGFKPKGVKVELKSKVGLFNALLEALLN 429

QY 438 YIVPILVLRVNEKLOKGFPLTPARVQLYNNVLOPHQNLFLFGADVY 477
```







```

Db 14 LSLLLAARPGALGT--NPGILITITDKGLAYAREGILLALQKLLVTLFDSGDGRK 70
Qy 76 HLKGHGYFYSMDIREFQLPSSQISMVNVGLKFSISNANIKISGKWAQK-R 127
Db 71 HFGRQYKFKYSLKIPRPELLRGTLRPLPGQGLSLDISDAVIHVRGSKVRKAFRLKNSF 130
Qy 136 DLSTEGHSISADLXGNSPTSGKPTITCSSSHSHINSVHVHISKSKVGLIQLPHKKIES 187
Db 131 DLYVKGITISVHLVLSGE-SGRPTVTTSKSSDIQNVELDI-EGDLEELNLLQSQIDA 188
Qy 196 ALRNKMSQVCEKVTNSVSSKQYFOTLPVMTKIDSVAGINGLVAPPATTATLTDVQM 255
Db 189 RLRLVLSKICRQIEEAVTAHLQYLPQLPTVTTQIDSFAGIDYLSMEAPRATAGMLDMVF 248
Qy 256 KGEFYSNHNHNPFPAPPVMEFPAADRMVYLGSLDYFFNTAGIYVQAGVLKWLTRDDM 315
Db 249 KGEIFPLDHRSPVDFLAPAMNLPKSHRSMVYFSDYVFNTASLAYHKSGVWNPSTIDAM 308
Qy 316 IPKESKRLTTKFRGTFLPEVAKFPNMKIQIHVSASTPPHLSVQPTGLTFYPADVQAF 375
Db 309 VPADLNIRRTTKSRPFPVLLANLYPNNLLEQTVNSEQLVNLSTENLLEPEMDIEAL 368
Qy 376 AVLPNSSLASFLTGHTTSGMEVSAESNRLVGLKLDRLLELKHGNIQPPFPVELLQDI 435
Db 369 VVLPSSAREPVRFGVATVNSATLITNTRKITGFKRQLVGLKESKVGFGFVELLEAL 428
Qy 436 MNYIVPILVPRVNEKLOKQFPPLTPARVQLYNNVLPQHNFLFGADVYK 487
Db 429 LNYVILNLYPKVNEKLAHRPPLRLRHQIQLYDLQLQTHENFLVAGNIQVR 480

RESULT 14
Q8JFX3 PRELIMINARY; PRT; 473 AA.
AC Q8JFX3
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DE LBP (LPS binding protein)/BPI (Bactericidal/permeability-increasing protein) like-2.
GN Name=LBP/BPI-2;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22018144; PubMed=12023361;
RA Inagawa H., Honda T., Kohchi C., Nishizawa T., Yoshiura Y., Nakanishi T., Yokomizo Y., Soma G.;
RT "Cloning and characterization of the homolog of mammalian lipopolysaccharide-binding protein and bactericidal permeability-increasing protein in rainbow trout Oncorhynchus mykiss.";
RL J. Immunol. 168:5638-5644(2002).
DR EMBL; AB042025; BAB91243.1; -.
DR HSSP; P17213; IEWF.
DR GO; GO:0008289; F:lipid binding; IEA.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP_1.
DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR SMART; SM00328; BPI1; 1.
DR SMART; SM00329; BPI2; 1.
SQ SEQUENCE 473 AA; 51262 MW; 00977A492EB09920 CRC64;

Query Match 34.7%; Score 870.5; DB 2; Length 473;
Best Local Similarity 35.3%; Pred. No. 1.5e-57;
Matches 169; Conservative 121; Mismatches 178; Indels 11; Gaps 6;

Qy 9 PCNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQTAALQKELKRIKIPDY 68
Db 3 PC-----CLLALLAV-ISLTLAASPGVKVKLTDKGIEYKQIGWASLQOQKLTWKVPDL 55

Qy 69 SDSFKIKHLKGHYSFYSDMDIREFQLPSSQISMVNVGLKFSISNANIKISGKWAQ-KR 127
Db 56 SGTEKVPPIGKVYISLTGMTIIVNLGPKSALVLMPTGTGVRLATINAFINLHGNWRVYFR 115
Qy 128 FLKMSGNFDLSIBGMSISADLXGNSPTSGKPTITCSSSHSHINSVHVHISKSKVGLIQL 187
Db 116 FIDRGSFDLAVNGLITADIAIKSDET-GRPTVSTVNCVANVSASIKF-HGASWLYN 173
Qy 188 LFHKKIESALRNKMSQVCEKVTNSVSSKQYFOTLPVMTKIDSVAGINGLVAPPATT 247
Db 174 LFKSYIDKALRSALQKICPLVAD-VITDMNPHLKTFNVLAKVDQVAEISYMSVTSPTIS 232
Qy 248 AETLDVQMKGEFYSNHNHNPFPAPPVMEFPAADRMVYLGSLDYFFNTAGIYVQAGVL 307
Db 233 KSSIEFSLGGEFYNIGKHQEPFSPFPFPPDNNMLYIGVSSFTNPSAGFTVNNAGAL 292
Qy 308 KMTLRDDMIPKESKRLTTKFRGTFLPEVAKFPNMKIQIHVSASTPPHLSVQPTGLTFY 367
Db 293 SLVYTDMMIPSSPIRLNTGTGFGVFEIPIAKRFGMMKLLVKTVEPTISLENNVTQ 352
Qy 368 PAVDQAFVLPNSSLASFLTGHTTSGMEVSAESNRLVGLKLDRLLELKHGNIQPP 427
Db 353 ASGTVTAYAIQPTNTLSPLFVLNMEGVSQAQMVTVGKLAGAITLKNKIEMTLGTSYVGQF 412
Qy 428 PVELLQDIMNYIYVILVPRVNEKLOKQFPPLTPARVQLYNNVLPQHNFLFGADVY 486
Db 413 QVQSLONIFLMLKLVVIVPKVNARLEKGPPLPTIGKNLINTQLQVLKDYMLIGTDVQF 471

RESULT 15
Q8JFX4 PRELIMINARY; PRT; 473 AA.
AC Q8JFX4
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE LBP (LPS binding protein)/BPI (Bactericidal/permeability-increasing protein)-1.
GN Name=LBP/BPI-1;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22018144; PubMed=12023361;
RA Inagawa H., Honda T., Kohchi C., Nishizawa T., Yoshiura Y., Nakanishi T., Yokomizo Y., Soma G.;
RT "Cloning and characterization of the homolog of mammalian lipopolysaccharide-binding protein and bactericidal permeability-increasing protein in rainbow trout Oncorhynchus mykiss.";
RL J. Immunol. 168:5638-5644(2002).
DR EMBL; AB042025; BAB91243.1; -.
DR HSSP; P17213; IEWF.
DR GO; GO:0008289; F:lipid binding; IEA.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP_1.
DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR SMART; SM00328; BPI1; 1.
DR SMART; SM00329; BPI2; 1.
SQ SEQUENCE 473 AA; 51430 MW; 3F9DF180695CA3D7 CRC64;

Query Match 34.6%; Score 867.5; DB 2; Length 473;
Best Local Similarity 35.1%; Pred. No. 2.5e-57;
Matches 168; Conservative 119; Mismatches 181; Indels 11; Gaps 6;

Qy 9 PCNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQTAALQKELKRIKIPDY 68
Db 3 PC---CWLALLAVPFF-----ALATNPGVKVKLTGKIEYKQIGWASLQOQKLTWKVPDL 55

Qy 69 SDSFKIKHLKGHYSFYSDMDIREFQLPSSQISMVNVGLKFSISNANIKISGKWAQ-KR 127

```

Db	56	SGTERVAPIGVKYSLTGITIVNGLPYSALALVPTDGISLSITNAFISLHGNWKIRYLS	115
Qy	128	FLKMSGFDSLIEGMSISADIKGSNPTSGKPTITCGSCSSHINSVHVHISKSXVGMLIQ	187
Db	116	FIKOSGFDLEVDGLTVTDSITIIKSDET-GRPTVSSVNCVANVGSASIKP-HGGASWLYN	173
Qy	188	LFHKKIESALRNKMNSQVCEKVTNSVSSKLOPYFQTLPMVTKIDSVAGINYGLVAPPATT	247
Db	174	LFSAYIDKALRSALQKQICPLVADTITD-MNPHLKTNLVLAKVDKYAEVEYSMTVSTIS	232
Qy	248	AETLDVQMKGEFYSENHHNPPFPVMEFFAAHDMVYLGSDYFFNTAGLVYQACVL	307
Db	233	NASIDFSLKGEFYNIKGHEPFPSPFSLPPQVNNMLYIGMSAFTTNSAGFVYNNAGAL	292
Qy	308	KWTLRDDMI PKESKFRLTTPKFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQPTGLTFY	367
Db	293	SLYITDDMI PPSPIRLNTRTFGAFIETAKRFFSMMKLVKTVKPTIFFEPNNVTIQ	352
Qy	368	PAVDVQAFVLPNSSLASFLIGMHTTGSMEVSAESNRLVGELKLDRLLELKHNSIGPF	427
Db	353	ASGSVTAYAIQPNITLSPFLVLMGESSVARSLYVTGVRLAGAVTLNKIEMTLETSYVGQF	412
Qy	428	PVELLDIMNIVIPILVLPVNEKLQGFPLPTPARVOLYNNVLQPHONFLFGADVY	486
Db	413	QVRSIDNIFLWLVKVAVIPKNARLEKGFPLPSIGKMNLVNTQLQVLKDYMLIGTDVQF	471

Search completed: October 21, 2005, 11:30:48  
Job time : 174.285 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2005, 11:22:43 ; Search time 14.2593 Seconds  
(without alignments)  
1241.566 Million cell updates/sec

Title: US-10-629-516-2\_COPY\_10\_193

Perfect score: 943  
Sequence: 1 CNAPRWWSMLVLAIGTAVT.....RVHISKSKVGWLIQLFHKKI 184

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	943	100.0	487	A30909	bactericidal/permeability-increasing protein precursor - human
2	832	88.2	250	S43383	bactericidal/permeability-increasing protein precursor - human
3	596.5	63.3	482	S10180	bactericidal/permeability-increasing protein precursor - human
4	430	45.6	481	A54136	lipopolysaccharide
5	428	45.4	481	I56246	lipopolysaccharide
6	416	44.1	477	A35843	lipopolysaccharide
7	357.5	37.9	482	B35843	lipopolysaccharide
8	172.5	18.3	493	I49370	plasma phospholipid
9	169	17.9	493	A35333	phospholipid trans
10	130.5	13.8	493	A28941	cholesterol ester
11	129.5	13.7	497	I46692	cholesterol ester
12	120.5	12.8	493	A53176	cholesterol ester
13	110	11.7	576	T22700	hypothetical protein
14	102	10.8	606	T23190	hypothetical protein
15	98.5	10.4	824	E87856	protein F10D11.6
16	98.5	10.4	846	T20710	hypothetical protein
17	95	10.1	488	C86183	hypothetical protein
18	92	9.8	464	T16889	hypothetical protein
19	90.5	9.6	486	T20482	hypothetical protein
20	89	9.4	827	D96907	phage-related protein
21	84.5	9.0	1169	G72571	probable DNA-direct
22	84	8.9	405	D84871	probable polygalactonate
23	82.5	8.7	498	B99946	hypothetical protein
24	82.5	8.7	573	S50627	hypothetical protein
25	82.5	8.7	218	B84683	hypothetical protein
26	82	8.7	554	T15438	hypothetical protein
27	82	8.7	1120	T38431	DNA-directed RNA p
28	81.5	8.6	1902	C97702	cell surface antigen
29	80	8.5	440	B71162	hypothetical protein

30	79.5	8.4	518	2	S73432	MG096 homolog D09-
31	79.5	8.4	869	2	T22422	hypothetical prote
32	79.5	8.4	1134	2	T04587	hypothetical prote
33	78.5	8.3	433	2	T03632	ornithine decarbox
34	78.5	8.3	2154	2	F83068	hypothetical prote
35	78	8.3	201	2	AG2778	conserved hypotet
36	78	8.3	201	2	C97558	hypothetical prote
37	78	8.3	274	2	T51714	probable formamido
38	78	8.3	390	2	E96565	hypothetical prote
39	78	8.3	390	2	T51713	probable formamido
40	78	8.3	766	2	S61424	inorganic diphosph
41	77.5	8.2	373	2	E90241	soluble hydrogenas
42	77.5	8.2	473	2	SL7448	probable ligand-bi
43	77.5	8.2	999	2	F72453	probable cytochrom
44	77	8.2	439	2	H71413	probable cucumisin
45	77	8.2	571	2	T12773	conserved hypotet

## ALIGNMENTS

### RESULT 1

A30909  
Bactericidal/permeability-increasing protein precursor - human  
N:Alternate names: SSK bactericidal protein

C:Species: Homo sapiens (man)  
C:Date: 18-Apr-1989 #sequence revision 18-Apr-1989 #text-change 09-Jul-2004  
C:Accession: A33850; B54136; A29464; A49716; A30909  
R:Gray, P.W.; Flaegge, G.; Leong, S.R.; Gumina, R.J.; Weiss, J.; Ooi, C.E.; Elsbach, P.  
J. Biol. Chem. 264, 9505-9509, 1989  
A:Title: Cloning of the cDNA of a human neutrophil bactericidal protein. Structural and  
A:Reference number: A33850; MUID:89255455; PMID:2722846  
A:Accession: A33850  
A:Molecule type: mRNA  
A:Residues: 1-487 <GRA>  
A:Cross-references: UNIPROT:Q9UCT4; GS:J04739; NID:gl79528; PID:AA51841.1; PID:gl79529  
R:Wilde, C.G.; Seilheimer, J.J.; McGrogan, M.; Ashton, N.; Snable, J.L.; Lane, J.C.; Leon  
J. Biol. Chem. 269, 17411-17416, 1994  
A:Title: Bactericidal/permeability-increasing protein and lipopolysaccharide (LPS)-bindi  
A:Reference number: A54136; MUID:94292492; PMID:7517398  
A:Accession: B54136  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-374, 'L', 376-487 <WIL>  
A:Experimental source: HL-60 cells  
A:Note: sequence extracted from NCBI backbone (NCBI:149855)  
R:Ooi, C.E.; Weiss, J.; Elsbach, P.; Frangione, B.; Mannion, B.  
J. Biol. Chem. 262, 14891-14894, 1987  
A:Title: A 25-KDa amino-terminal fragment carries all the antibacterial activities of th  
A:Reference number: A29464; MUID:88033057; PMID:3667613  
A:Accession: A29464  
A:Molecule type: protein  
A:Residues: 32-51 <OOI>  
A:Experimental source: neutrophils  
R:Wasilik, K.R.; Skubitz, K.M.; Gray, B.H.  
Infect. Immun. 59, 4193-4200, 1991  
A:Title: Comparison of granule proteins from human polymorphonuclear leukocytes which ar  
A:Reference number: A43600; MUID:92040097; PMID:1937776  
A:Accession: A43600  
A:Molecule type: protein  
A:Residues: 32-52, 'R' <WAS>  
R:Little, R.G.; Kellner, D.N.; Lim, E.; Burke, D.J.; Conlon, P.J.  
J. Biol. Chem. 269, 1865-1872, 1994  
A:Title: Functional domains of recombinant bactericidal/permeability increasing protein  
A:Reference number: A49716; MUID:94124531; PMID:8294435  
A:Accession: A49716  
A:Molecule type: protein  
A:Residues: 32-130, 132-141, 143-165, 202-215, 'E', 217-225 <LIT>  
C:Comment: The bactericidal/permeability-increasing protein (BPI) is a 60 kD membrane-as  
which is specific for gram-negative bacteria. BPI has a high affinity for lipopolysaccha  
between BPI and an LPS-binding protein from liver and cholesterol ester transfer protein  
C:Genetics:  
A:Gene: GDB:BPI

A;Cross-references: GDB:131572; OMIM:109195  
A;Map Position: 20q11.23-20q12  
C;Superfamily: lipopolysaccharide-binding protein  
C;Keywords: antibacterial; cytotoxin; glycoprotein; heparin binding; neutrophil  
F;1-31/Domain: signal sequence #status predicted <SIG>  
F;32-487/Product: bactericidal permeability-increasing protein #status predicted <MAT>  
F;32-51/Region: bactericidal #status predicted  
F;380/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 943; DB 2; Length 487;  
Best Local Similarity 100.0%; Pred. No. 1e-77;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNAPRWVSLMVLVAIGTAVTAANVPGVVRISQKGLDYASQOQTAAALQKELKRIKIPDYS 60  
DB 10 CNAPRWVSLMVLVAIGTAVTAANVPGVVRISQKGLDYASQOQTAAALQKELKRIKIPDYS 69  
QY 61 DSKFKHLGKHGHSFYFSDIREFOLPSSQISMPVNVGLKFSISNANIKISGKWAQKRF 120  
DB 70 DSKFKHLGKHGHSFYFSDIREFOLPSSQISMPVNVGLKFSISNANIKISGKWAQKRF 129  
QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKVGWLIQLF 180  
DB 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKVGWLIQLF 189  
QY 181 HKKI 184  
DB 190 HKKI 193

RESULT 2  
S43383  
bactericidal/permeability-increasing protein - synthetic  
C;Species: synthetic  
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C;Date: 20-Oct-1994 #sequence\_revision 15-Feb-1996 #text\_change 15-Feb-1996  
C;Accession: S43383  
R;Qi, S.Y.; Li, Y.; O'Connor, C.D.  
Biochem. J. 298, 711-718, 1994  
A;Title: The region around residue 115 of human bactericidal/permeability-increasing protein of a gene coding for the active domain and characterization of recombinant proteins.  
A;Reference number: S43383  
A;Accession: S43383  
A;Molecule type: DNA  
A;Residues: 1-250 <QIS>

Query Match 88.2%; Score 832; DB 4; Length 250;  
Best Local Similarity 100.0%; Pred. No. 5.4e-68;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 VNPGVVVRISQKGLDYASQOQTAAALQKELKRIKIPDYSDFKIKHLGKHGHSFYFSDIRE 82  
DB 2 VNPGVVVRISQKGLDYASQOQTAAALQKELKRIKIPDYSDFKIKHLGKHGHSFYFSDIRE 61  
QY 83 FQLPSSQISMPVNVGLKFSISNANIKISGKWAQKRFKMSGNFDLSIEGMSISADLKL 142  
DB 62 FQLPSSQISMPVNVGLKFSISNANIKISGKWAQKRFKMSGNFDLSIEGMSISADLKL 121  
QY 143 SNPTSGKPTITCSCSSHNSVHVHISKVGWLIQLFHKKI 184  
DB 122 SNPTSGKPTITCSCSSHNSVHVHISKVGWLIQLFHKKI 163

RESULT 3  
S10180  
bactericidal permeability-increasing protein precursor - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004  
C;Accession: S10180  
R;Leong, S.R.; Camerato, T.  
Nucleic Acids Res. 18, 3052, 1990  
A;Title: Nucleotide sequence of the bovine bactericidal permeability increasing protein  
A;Reference number: S10180; MUID:90272418; PMID:2349103

A;Accession: S10180  
A;Molecule type: mRNA  
A;Residues: 1-482 <LEO>  
A;Cross-references: UNIPROT:P17453; EMBL:X52563; NID:g138; PIDN:CAA36797.1; PID:g139  
C;Superfamily: lipopolysaccharide-binding protein  
F;1-26/Domain: signal sequence #status predicted <SIG>  
F;27-482/Product: bactericidal permeability increasing protein #status predicted <MAT>

Query Match 63.3%; Score 596.5; DB 2; Length 482;  
Best Local Similarity 63.3%; Pred. No. 2.8e-46;  
Matches 115; Conservative 29; Mismatches 37; Indels 1; Gaps 1;

QY 3 APRWVSLMVLVAIGTAVTAANVPGVVRISQKGLDYASQOQTAAALQKELKRIKIPDYS 62  
DB 8 ARWATLVLAALGTAVT-TTNGIVARITQGLDYACQGVLTLOKELEKTIIPNPSGN 66  
QY 63 FKIKHLGKHGHSFYFSDIREFOLPSSQISMPVNVGLKFSISNANIKISGKWAQKRF 122  
DB 67 FKIKYLGKGYSPFPMVIOGFNLPNSQIRPLPKGLDLSIRDASIKIRGKWKARKNFIKL 126  
QY 123 SGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKVGWLIQLFHK 182  
DB 127 GGNFDLSVEGISLAGNLGYDPASGHSTVTCSSSGINTVRIHISGSLGWLIIQLFR 186  
QY 183 KI 184  
DB 187 RI 188

RESULT 4  
A54136  
lipopolysaccharide-binding protein - human  
N;Alternate names: LBP; LPS-binding protein  
C;Species: Homo sapiens (man)  
C;Date: 11-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A54136  
R;Wilde, C.G.; Seilhamer, J.J.; McGrogan, M.; Ashton, N.; Snable, J.L.; Lane, J.C.; Leon  
J. Biol. Chem. 269, 17411-17416, 1994  
A;Title: Bactericidal/permeability-increasing protein and lipopolysaccharide (LPS)-binding protein  
A;Reference number: A54136  
A;Accession: A54136  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-481 <WIL>  
A;Cross-references: UNIPROT:P18428  
A;Experimental source: liver  
A;Note: sequence extracted from NCBI backbone (NCBIP:149401)  
C;Superfamily: lipopolysaccharide-binding protein

Query Match 45.6%; Score 430; DB 2; Length 481;  
Best Local Similarity 46.6%; Pred. No. 3.5e-31;  
Matches 82; Conservative 38; Mismatches 54; Indels 2; Gaps 2;

QY 9 LMVLVAIGTAVTAANVPGVVRISQKGLDYASQOQTAAALQKELKRIKIPDYSFKIKHL 68  
DB 12 LLALLLTSTPCALGANFGLVARITDKGLQYAAQEGLLALQSELLRITLPDFTGDLRPHV 71  
QY 69 GKGHYFYSMDIREFOLPSSQISMPVNVGLKFSISNANIKISGKWAQKRFKMSGNFDL 128  
DB 72 GRGRYEFHSLNIHSCCELLSALRPVPGQLSLISDSSIRVQGRWKVKRFFKLQGSFDV 131  
QY 129 SIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKVGWLIQLFHKKI 184  
DB 132 SVKGISISVNLLOSP-SSGRPTVTASSCSSDADIADVEVMS-GDLGLWLLNLFHNQI 185

RESULT 5  
I56246  
lipopolysaccharide binding protein - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I56246  
R;Su, G.L.; Freeswick, P.D.; Geller, D.A.; Wang, Q.; Shapiro, R.A.; Wan, Y.H.; Billiar, J.

J. Immunol. 153, 743-752, 1994  
A:Title: Molecular cloning, characterization, and tissue distribution of rat lipopolysaccharide-binding protein (LBP)  
A:Reference number: I56246; MUID:94292804; PMID:8021509  
A:Accession: I56246  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-481 <RES>  
A:Cross-references: UNIPROT:Q63313; GB:I32132; NID:G510714; PIDN:AAA21835.1; PID:G510715  
C:Superfamily: lipopolysaccharide-binding protein

Query Match 45.4%; Score 428; DB 2; Length 481;  
Best Local Similarity 44.2%; Pred. No. 5.4e-31;  
Matches 80; Conservative 45; Mismatches 54; Indels 2; Gaps 2;  
QY 4 PRWSLMVLVAIGTAVTAANPVGVRISQKGLDYASOQGTAAALQKELKRIKIPDYSDF 63  
DB 7 PLLPTLLGLLLSIPRTQGNPAMVVRITDKGLEVAKEGLLSLQRELYKITLPDPSGDF 66  
QY 64 KIKHLGKHYSFYSDIREFOLPSSQISWPNVGLKFSISNANIKISGKWAQKRFKMS 123  
DB 67 KIKAVGRQGYEFHSLIEQSCQLRGSLSKPLPGRGLSLSDSSISVGRGKWKVRRSFVKLH 126  
QY 124 GNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSHINSVHVHISKVKWGLIOLPHKK 183  
DB 127 GSFDLGVKSVTISVDLLGLGVDP-SERPVTATAGCSNRIRDELHVS-GNVGMLLNFHQ 184  
QY 184 I 184  
DB 185 I 185

RESULT 6  
A35843  
lipopolysaccharide-binding protein - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Oct-1990 #sequence\_revision 05-Oct-1990 #text\_change 09-Jul-2004  
C:Accession: A35843  
R:Schumann, R.R.; Leong, S.R.; Gray, G.W.; Wright, S.D.; Mathison, J.C.; T  
Science 249, 1429-1431, 1990  
A:Title: Structure and function of lipopolysaccharide binding protein.  
A:Reference number: A35843; MUID:90385281; PMID:2402637  
A:Accession: A35843  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-477 <SCH>  
A:Cross-references: UNIPROT:P18428; GB:M35533; NID:G186965; PIDN:AAA59493.1; PID:G186968  
C:Genetics:  
A:Gene: GDB:LBP  
A:Cross-references: GDB:I31571; OMIM:151990  
A:Map position: 20q11.23-20q12  
C:Superfamily: lipopolysaccharide-binding protein

Query Match 44.1%; Score 416; DB 2; Length 477;  
Best Local Similarity 46.0%; Pred. No. 6.5e-30;  
Matches 81; Conservative 36; Mismatches 57; Indels 2; Gaps 2;  
QY 9 LMLVLAIGTAVTAANPVGVRISQKGLDYASOQGTAAALQKELKRIKIPDYSDFKIKHL 68  
DB 12 LLALLTSTPEALGANPGLUVAITDKGLQYAAQEGLLALQSELLRITLPDFTGDIRPHV 71  
QY 69 KGKHSFYSDIREFOLPSSQISWPNVGLKFSISNANIKISGKWAQKRFKMSGNFDL 128  
DB 72 GRGRYEFHSLNHSCELLHSALRPVPGQGLSLSDSSISRVQGRWKVRSFFKLGSGFDV 131  
QY 129 STEGMSISADLKLGSNPTSGKPTITCSSSHINSVHVHISKVKWGLIOLPHKKI 184  
DB 132 SVKGISISVNLGLSE-SSGRPTGYCLSCSSDIADVEVDMGDS-GWLLNLFHQI 185

RESULT 7  
B35843  
lipopolysaccharide-binding protein - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 05-Oct-1990 #sequence\_revision 05-Oct-1990 #text\_change 09-Jul-2004  
C:Accession: B35843; A46553  
R:Schumann, R.R.; Leong, S.R.; Flaggs, G.W.; Gray, P.W.; Wright, S.D.; Mathison, J.C.; T  
Science 249, 1429-1431, 1990  
A:Title: Structure and function of lipopolysaccharide binding protein.  
A:Reference number: A35843; MUID:90385281; PMID:2402637  
A:Accession: B35843  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-482 <SCH>  
A:Cross-references: UNIPROT:P17454; GB:M35534; NID:G165467; PIDN:AAA99235.1; PID:G165468  
R:Tobias, P.S.; Soldau, K.; Ulevitch, R.J.  
J. Exp. Med. 164, 777-793, 1986  
A:Title: Isolation of a lipopolysaccharide-binding acute phase reactant from rabbit seru  
A:Reference number: A46553; MUID:86306528; PMID:2427635  
A:Accession: A46553  
A:Molecule type: protein  
A:Residues: 27-55, 'XG', 58-62, 'P', 64-65 <TOB>  
C:Superfamily: lipopolysaccharide-binding protein  
C:Keywords: acute phase

Query Match 37.9%; Score 357.5; DB 2; Length 482;  
Best Local Similarity 41.0%; Pred. No. 1.3e-24;  
Matches 73; Conservative 39; Mismatches 61; Indels 5; Gaps 3;  
QY 7 VSLMVLVAIGTAVTAANPVGVRISQKGLDYASOQGTAAALQKELKRIKIPDYSDFKIK 66  
DB 14 LSLLLAAAPGALGT---NPGILTRITDKGLEVAAREGLLALQKLELTLTPDSGDGDFRIK 70  
QY 67 HLGRGHYSFYSDIREFOLPSSQISWPNVGLKFSISNANIKISGKWAQKRFKMSGNF 126  
DB 71 HFGRAQYKFSYSLKIPRFELLGRTLRPLPGQGLSLDISDAYIHVRGSKVRKAFRLKMSF 130  
QY 127 DLSIEGMSISADLKLGSNPTSGKPTITCSSSHINSVHVHISKVKWGLIOLPHKKI 184  
DB 131 DLYKGLTISVHLVLGSE-SSGRPTVTSSCSDIQNVELDI-EGDLELLNLLSQI 186

RESULT 8  
I49370  
plasma phospholipid transfer protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I49370  
R:Albers, J.J.; Wolfbauer, G.; Cheung, M.C.; Day, J.R.; Ching, A.F.; Lok, S.; Tu, A.Y.  
Biochim. Biophys. Acta 1258, 27-34, 1995  
A:Title: Functional expression of human and mouse plasma phospholipid transfer protein.  
A:Reference number: I49370; MUID:95383401; PMID:7654777  
A:Accession: I49370  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-493 <RES>  
A:Cross-references: UNIPROT:P55065; EMBL:U37226; NID:G1051265; PIDN:AAA80542.1; PID:G1051265  
C:Superfamily: lipopolysaccharide-binding protein

Query Match 18.3%; Score 172.5; DB 2; Length 493;  
Best Local Similarity 28.8%; Pred. No. 8.4e-08;  
Matches 47; Conservative 40; Mismatches 63; Indels 13; Gaps 4;  
QY 9 LMLVLAIGTAVTAANV---PGVVVRISQKGLDYASOQGTAAALQKELKRIKIPDYSDFKI 65  
DB 1 MYLLWALFLALLAGAHAEPLGCKIRVTSAALDLVKQEGRLFLEQLETTITPDV----- 54  
QY 66 KHLGKHYSFYSDIR--EPQLPSSQISWPNVGLKFSISNANIKISGKWAQKRFKMS 123  
DB 55 YGAKGHFYNYISDVVRVQLHLISSELHFQPDQDLLLLNISNLASGLHFRQLLYWFLYDG 113  
QY 124 GNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSHINSVHV 166  
DB 114 GYNASAEVSIKRTGLQL-SQDSSGRIKVSNVSCASVSQNMN 155

RESULT 9





QY 143 SNPT--SGKPTTTCSSSHNSVHVI-SKSKVGLIQLF 180  
 Db 144 TOLTCDGRVTRDAPDCVLSFHKLHLHQLGEREPQIKOLF 184

RESULT 13  
 T22700  
 hypothetical protein F55B12.5 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T22700  
 R:Sims, M.  
 submitted to the EMBL Data Library, September 1996  
 A:Reference number: Z19602  
 A:Accession: T22700  
 A:Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: DNA  
 A:Residues: 1-576 <WIL>  
 A:Cross-references: UNIPROT:Q93796; EMBL:Z79757; PIDN:CAB02126.1; GSPDB:GN00023; CESP:F55B12  
 A:Experimental source: clone F55B12  
 C:Genetics:  
 A:Gene: CESP:F55B12.5  
 A:Map position: 5  
 A:Introns: 47/1; 147/3; 178/3; 290/3; 353/2; 384/2; 427/3  
 C:Superfamily: Caenorhabditis elegans hypothetical protein F55B12.5

Query Match 11.7%; Score 110; DB 2; Length 576;  
 Best Local Similarity 22.9%; Pred. No. 0.048; 76; Indels 22; Gaps 5;  
 Matches 38; Conservative 30; Mismatches 76; Indels 22; Gaps 5;

QY 9 LMLVVAIGTAVTAA-----VNPQGVVVRISQKGLDYASQOQTAAQKELKRIKIPD-YSDSF 63  
 Db 11 LVSIITQVGNADSSEITHKPAIGYVRLNQXAVDYVADLASDALPALNNLSPDIVTDM 70

QY 64 KIKHKGKHYSPYMDIREFQPSQISMVNPGVKFSISNANIKISGWKAKQKPLKMS 123  
 Db 71 KITKL-----HISNVAKPNLSAKFIDGKGVAYNISLASFRASAYAEISVFVMSYE 120

QY 124 GNFDLSIEGMSADLKLSGNTSGKPTTTCSSSHNSVHVI 169  
 Db 121 GDPTAELRELSIELHFDYN---GTTVNASVC-----NVTHSELS 159

RESULT 14  
 T29190  
 hypothetical protein C55C3.1 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T29190  
 R:Woessne, J.; Stellyes, L.  
 submitted to the EMBL Data Library, April 1996  
 A:Description: The sequence of C. elegans cosmid C55C3.  
 A:Reference number: Z20585  
 A:Accession: T29190  
 A:Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: DNA  
 A:Residues: 1-606 <WOE>  
 A:Cross-references: UNIPROT:Q18869; EMBL:U53335; PIDN:AAA96173.1; GSPDB:GN00022; CESP:C55C3  
 A:Experimental source: strain Bristol N2; clone C55C3  
 C:Genetics:  
 A:Gene: CESP:C55C3.1  
 A:Map position: 4  
 A:Introns: 61/3; 99/2; 126/2; 161/3; 283/2; 359/2; 424/1; 463/3; 522/1; 570/1

Query Match 10.8%; Score 102; DB 2; Length 606;  
 Best Local Similarity 24.5%; Pred. No. 0.27;  
 Matches 47; Conservative 33; Mismatches 76; Indels 36; Gaps 10;

QY 1 CNAPRWVSLMVLVAIGTAVT-----AAVN--PGVVRISQKGLDYASQOG 43  
 Db 5 CN-QNPPSFLILVASALFITFIGSIDSEHNFHLLAAPTLPFGVRVRLPRLGLAYLNHLA 63

QY 44 TAAQKELKRIKIPDYS-----DSFKIKHLKGKHYSFYSMDIREFQPSQISMVNPGVK 99  
 Db 64 ANLLAQQLPRLILPDVEHILPSNQGIYISKVLHSRFR--AEHHQLNST----APN-KIS 117

QY 100 FSIISNANIKISGWKAKQKRF--LKMSGNFOLDSTEGMS--ISADLKLSGNTSGKPTTTC 154  
 Db 118 WTMQMDIGLGLDLSGSVNIVVPLNTQGVILAQGLTFHLESSEIEKGN---GSAKVTS 174

QY 155 SSCSSHNSVHV 166  
 Db 175 LSCLATIRDTV 186

RESULT 15  
 E87856  
 protein F10D11.6 [imported] - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
 C:Accession: E87856  
 R:Anonymous, The C. elegans Sequencing Consortium.  
 Science 282, 2012-2018, 1998  
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
 A:Reference number: A75000; MUID:99069613; PMID:9851916  
 A:Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_elegans/  
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
 A:Accession: E87856  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-824 <STO>  
 A:Cross-references: UNIPROT:O17781; GB:chr\_I; PIDN:CAB02917.1; PID:G3875779; GSPDB:GN000  
 C:Genetics:  
 A:Gene: F10D11.6  
 A:Map position: 1

Query Match 10.4%; Score 98.5; DB 2; Length 824;  
 Best Local Similarity 21.6%; Pred. No. 0.81; 78; Indels 9; Gaps 4;  
 Matches 32; Conservative 29; Mismatches 29; Indels 9; Gaps 4;

QY 25 PGVVRISQKGLDYASQOQTAAQKELKRIKIPDYSDFSFKIKHLKGKHYSFYSMDIREFQ 84  
 Db 39 FGLRLARLSRAFYASTLVGGILNTEIKKARIPPIISQCIP---WVQGVNIYNLYSVRYR 95

QY 85 LPSSQISM-VPNVGLKFSISNANIKISGWKAKQKRF---KMSGNFDLSIEGMSISADLK 140  
 Db 96 CPQRVLYPAPENRIVLQVNVLDGVTGNLGGQIVVLLPILALSGIVQLNHOATITVQLA 155

QY 141 LGSNPTSGKPTTTCSSSHNSVHVI 168  
 Db 156 IERGRG--PYVRLUSCDMQIGYADAYI 181

Search completed: October 21, 2005, 11:31:49  
 Job time : 16.2593 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2005, 11:22:38 ; Search time 170.559 Seconds  
(without alignments)  
1104.324 Million cell updates/sec

Title: US-10-629-516-2

Perfect score: 2507

Sequence: 1 MRENARGPCNAPRWSLMV.....NVVLQPHNQLFLGADVVK 487

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2507	100.0	487	1	AAU06198 Human bac
2	2507	100.0	487	2	Aar44420 PING4512
3	2507	100.0	487	2	Aar62370 Recombina
4	2507	100.0	487	2	Aar57901 Bacterici
5	2507	100.0	487	2	Aar62344 Recombina
6	2507	100.0	487	2	Aar68923 Bacterici
7	2507	100.0	487	2	Aar79185 Recombina
8	2507	100.0	487	2	Aar79021 Bacterici
9	2507	100.0	487	2	Aar81247 Recombina
10	2507	100.0	487	2	Aar80995 Bacterici
11	2507	100.0	487	2	Aar67998 Holoprote
12	2507	100.0	487	2	Aar86455 rBPI for
13	2507	100.0	487	2	Aar76243 Recombina
14	2507	100.0	487	2	Aar05852 Recombina
15	2507	100.0	487	2	Aar97568 Human bac
16	2507	100.0	487	2	Aaw17987 Bacterici
17	2507	100.0	487	2	Aaw44550 Human bac
18	2507	100.0	487	2	Aaw01702 Human bac
19	2507	100.0	487	2	Aaw17986 Human bac
20	2507	100.0	487	2	Aaw47090 Human bac
21	2507	100.0	487	2	Aaw40141 Human rec
22	2507	100.0	487	2	Aaw61158 Recombina
23	2507	100.0	487	2	Aaw56156 A bacteri
24	2507	100.0	487	2	Aaw26776 Human bac
25	2507	100.0	487	2	Aaw63306 Recombina

26	2507	100.0	487	2	AAW63304 Human bac
27	2507	100.0	487	2	AAW41359 Human bac
28	2507	100.0	487	2	AAW94284 Human bac
29	2507	100.0	487	2	Aay17864 Human bac
30	2507	100.0	487	2	Aay31621 Human bac
31	2507	100.0	487	2	Aay26930 Recombina
32	2507	100.0	487	2	AAW98885 Human bac
33	2507	100.0	487	3	AAY51169 Human BPI
34	2507	100.0	487	3	AAY88382 Human bac
35	2507	100.0	487	3	AAB16109 Human bac
36	2507	100.0	487	3	AAB16184 Recombina
37	2507	100.0	487	3	AAY68319 Human bac
38	2507	100.0	487	3	AB03943 Bacterici
39	2507	100.0	487	3	AB18762 A human b
40	2507	100.0	487	3	AAW07751 A human b
41	2507	100.0	487	3	AB11117 Human BPI
42	2507	100.0	487	3	AB13335 Human BPI
43	2507	100.0	487	4	Aae09357 Human rBP
44	2507	100.0	487	4	AAY97625 Human BPI
45	2507	100.0	487	4	AAE01016 Recombina

ALIGNMENTS

RESULT 1	
AAU06198	
ID	AAU06198 standard; protein; 487 AA.
XX	
XX	AAU06198;
XX	
XX	16-JAN-2002 (first entry)
DT	
XX	Human bactericidal/permeability-increasing (BPI) protein.
DE	
XX	Human; bactericidal permeability-increasing protein; BPI; PMN;
XX	polymorphonuclear leukocyte; Gram-negative bacteria; bacteraemia; sepsis;
KW	bacterial infection; skin infection; decubitus ulcer; burn; vulnerary;
KW	antimicrobial; antibacterial; immunosuppressive; protein therapy.
XX	
XX	Homo sapiens.
OS	
XX	
XX	Key
FH	Location/Qualifiers
FT	1..31
FT	/label= Signal_peptide
FT	32..487
FT	/label= Mature BPI protein
FT	

XX CC The present invention relates to the isolation of human  
 CC bactericidal/permeability-increasing (BPI) protein from polymorphonuclear  
 CC leukocytes (PMN). BPI can be produced by growing in a culture medium,  
 CC host cells transformed or transfected to express BPI encoded by  
 CC nucleotides 124-1491 of the BPI polynucleotide sequence or its  
 CC complementary strand, or a human BPI DNA sequence that hybridizes under  
 CC stringent hybridization conditions with the BPI polynucleotide sequence  
 CC or its complementary strand. BPIs are useful against a wide range of Gram  
 CC -negative bacteria, particularly for the treatment of diseases caused by  
 CC Gram-negative bacteria such as bacteraemia or sepsis, infections caused  
 CC by Escherichia coli, Salmonella, Klebsiella or Pseudomonas, and skin  
 CC infections which occur in bedridden patients suffering from decubitus  
 CC ulcers (bed sores) or in burn patients. They can also be used as a model  
 CC for the design of new antibiotic agents, to provide sequence information  
 CC on BPI to direct the design of future generations of antimicrobial agents  
 CC specific for Gram-negative bacteria, and to be used as probes in  
 CC molecular biological techniques. The BPI protein sequence is also useful  
 CC in protein therapy. The present sequence represents the human BPI protein  
 CC of the present invention  
 XX CC  
 XX Sequence 487 AA;

Query Match 100.0%; Score 2507; DB 1; Length 487;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
 Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRSQKGLDYASQGGTAALQKEL 60  
 Db 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRSQKGLDYASQGGTAALQKEL 60

Qy 61 KRKIPDYSDFKIKHLGKHGHSFYSDMIREFOLPSSQISMVNPVGLKFSISNANIKISG 120  
 Db 61 KRKIPDYSDFKIKHLGKHGHSFYSDMIREFOLPSSQISMVNPVGLKFSISNANIKISG 120

Qy 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHISKS 180  
 Db 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHISKS 180

Qy 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLPQYFQTLPMVTKIDSVAGINYL 240  
 Db 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLPQYFQTLPMVTKIDSVAGINYL 240

Qy 241 VAPPATTAETLDVQMGKEFYSENHNPFPAPPVMEFPAAHDMVYLGSLDYFPNTAGLV 300  
 Db 241 VAPPATTAETLDVQMGKEFYSENHNPFPAPPVMEFPAAHDMVYLGSLDYFPNTAGLV 300

Qy 301 YQEAGVLKMTLRDDMI PKESKFRITTKFFCTFLPEVAKFPNKKIQIHVSASTPPHLSVQ 360  
 Db 301 YQEAGVLKMTLRDDMI PKESKFRITTKFFCTFLPEVAKFPNKKIQIHVSASTPPHLSVQ 360

Qy 361 PTGLTFFPAVDVQAFVLPNSSLASFLIGHHTTGSMEVSAESNRLVGBELKLDRLLELK 420  
 Db 361 PTGLTFFPAVDVQAFVLPNSSLASFLIGHHTTGSMEVSAESNRLVGBELKLDRLLELK 420

Qy 421 HSNIGPPFVELLDIMNVIYPIILVPRVNEKLQGFPLPTPARVOLNVLQPHQNFLLF 480  
 Db 421 HSNIGPPFVELLDIMNVIYPIILVPRVNEKLQGFPLPTPARVOLNVLQPHQNFLLF 480

Qy 481 GADVYK 487  
 Db 481 GADVYK 487

RESULT 2  
 AAR44420

ID AAR44420 standard; protein; 487 AA.

XX AC AAR44420;

XX DT 25-MAR-2003 (revised)

DT 03-JUN-1994 (first entry)

XX

DE DE PING4512 encoded fusion protein.  
 XX  
 XX Polymerase chain reaction; primer; amplify; PCR; plasmid; PING4512;  
 KW PING4503; bactericidal/permeability-increasing protein; BPI; IgG; heavy;  
 KW chain; pMB27; fusion protein; Gram negative; renal failure;  
 KW bacterial infection; endotoxin related shock; metabolic acidosis;  
 KW disseminated intravascular coagulation; anemia; thrombocytopenia;  
 KW leukopenia; adult respiratory distress syndrome; hypotension; fever;  
 KW constant region; lipopolysaccharide complement binding;  
 KW placental transfer; Fc receptor binding.  
 XX  
 XX Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT Peptide 1..31 "Signal peptide"  
 FT Protein 32..487  
 FT /note= "Mature rBPI (191)-IgG fusion protein"  
 XX  
 XX WO9323434-A2.  
 XX  
 XX 25-NOV-1993.  
 XX  
 XX 19-MAY-1993; 93WO-US004754.  
 XX  
 XX 19-MAY-1992; 92US-00885911.  
 XX  
 XX (XOMA ) XOMA CORP.  
 PA  
 XX Theofan G, Grinna LS, Horwitz A;  
 PI  
 XX WPI; 1993-386485/48.  
 DR N-PSDB; AAQ52488.  
 DR  
 XX New fusion proteins for treating bacterial infections - comprising a  
 PT bactericidal-permeability-increasing protein and a immunoglobulin heavy  
 PT chain constant domain.  
 PT  
 XX Claim 20; Page 48-50; 75pp; English.  
 PS  
 XX This sequence is encoded by the plasmid PING4512. PING4512 was  
 CC constructed using the primer sequence given in AAQ52480. Plasmid PING4503  
 CC was cut with AlwNI, the ends made blunt with T4 DNA polymerase, and the  
 CC DNA then cut with SalI. The resultant approx. 700bp SalI/blunt fragment  
 CC contains the 30 bp 5' untranslated region and the DNA encoding the signal  
 CC peptide and first 191 amino acids of bactericidal/permeability-increasing  
 CC protein (BPI). IgG heavy chain (HC) sequences, which also included the  
 CC hinge region of the IgG HC were PCR amplified from plasmid pMB27 using  
 CC these primers. Plasmids such as PING4512 may be used to produce fusion  
 CC proteins which are useful for the treatment of Gram negative bacterial  
 CC infections and their sequelae including endotoxin related shock and  
 CC conditions associated with it, such as disseminated intravascular  
 CC coagulation, anemia, thrombocytopenia, leukopenia, adult respiratory  
 CC distress syndrome, renal failure, hypotension, fever and metabolic  
 CC acidosis. Providing BPI or a fragment of it, as part of the fusion with an  
 CC immunoglobulin heavy chain constant region provides the potential  
 CC advantages of Fc receptor binding, bivalent binding to lipopoly-  
 CC saccharide complement binding and increasing placental transfer. (Updated  
 CC on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 487 AA;

Query Match 100.0%; Score 2507; DB 2; Length 487;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
 Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRSQKGLDYASQGGTAALQKEL 60  
 Db 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRSQKGLDYASQGGTAALQKEL 60

Qy 61 KRKIPDYSDFKIKHLGKHGHSFYSDMIREFOLPSSQISMVNPVGLKFSISNANIKISG 120  
 Db 61 KRKIPDYSDFKIKHLGKHGHSFYSDMIREFOLPSSQISMVNPVGLKFSISNANIKISG 120

QY 121 KWKAQKFLKMSGNFSLIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180  
 DB 121 KWKAQKFLKMSGNFSLIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180  
 QY 181 KVGWLIQLFHKKIESALRNKNSQVCEKVTNSVSKLPQYFOTLPVMTKIDS VAGINYL 240  
 DB 181 KVGWLIQLFHKKIESALRNKNSQVCEKVTNSVSKLPQYFOTLPVMTKIDS VAGINYL 240  
 QY 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEPPAAHDMVYLGLSDYFFNTAGLV 300  
 DB 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEPPAAHDMVYLGLSDYFFNTAGLV 300  
 QY 301 YQEAGVLKMTLRDDMI PKESKFRLLTTFKFGTFLPEVAKKFNPMKIQIHVSASTPPHLSVQ 360  
 DB 301 YQEAGVLKMTLRDDMI PKESKFRLLTTFKFGTFLPEVAKKFNPMKIQIHVSASTPPHLSVQ 360  
 QY 361 PTGLTFFPAVDVQAFVLPNSLSASLFLIGHMTTGSMEVSAESNRLVGLKLDRLLELK 420  
 DB 361 PTGLTFFPAVDVQAFVLPNSLSASLFLIGHMTTGSMEVSAESNRLVGLKLDRLLELK 420  
 QY 421 HSNIGPPFVELLQDIMNVIIVLPVPRVNEKLGKGFPLTPARVOLXNVVLQPHONFLF 480  
 DB 421 HSNIGPPFVELLQDIMNVIIVLPVPRVNEKLGKGFPLTPARVOLXNVVLQPHONFLF 480  
 QY 481 GADVYK 487  
 DB 481 GADVYK 487

RESULT 3  
 AAR62370  
 ID AAR62370 standard; protein; 487 AA.  
 AC AAR62370;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 27-APR-1995 (first entry)  
 DE Recombinant bactericidal/permeability-increasing protein (rBPI-50).  
 KW N-terminal; recombinant; bactericidal/permeability protein; rBPI;  
 KW signal protein; human; rBPI-23; binding assay; heparin-binding; domain;  
 KW Limulus amoebocyte lysate; LAL; inhibition; bactericidal activity;  
 KW chronic inflammatory disease; arthritis; psoriasis; Crohn's disease;  
 KW inflammatory bowel disease; asthma.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT Peptide  
 FT Location/Qualifiers  
 FT 1..31  
 FT /note= "Signal peptide"  
 FT Domain  
 FT 17..55  
 FT /note= "LAL inhibiting domain"  
 FT Binding-site  
 FT 21..55  
 FT /note= "Heparin binding site"  
 FT Protein  
 FT 32..487  
 FT /note= "mature protein"  
 FT Binding-site  
 FT 65..107  
 FT /note= "Heparin binding site"  
 FT Domain  
 FT 73..99  
 FT /note= "LAL inhibiting domain"  
 FT Active-site  
 FT 95..99  
 FT /note= "Bactericidally active fragment"  
 FT Binding-site  
 FT 137..171  
 FT /note= "Heparin binding site"  
 FT Domain  
 FT 137..163  
 FT /note= "LAL inhibiting domain"  
 XX  
 PN WO9420128-A1  
 XX  
 PD 15-SEP-1994.  
 XX

PF 11-MAR-1994; 94WO-US002401.  
 XX 12-MAR-1993; 93US-00030644.  
 PR 15-JUL-1993; 93US-00093202.  
 XX  
 PA (XOMA ) XOMA CORP.  
 XX  
 FI Little RG, Gazzanosantoro H, Parent JB;  
 XX N-PSDB; AAQ73382.  
 DR WPI; 1994-302679/37.  
 XX N-PSDB; AAQ73382.  
 DR  
 XX  
 FT Uses of bactericidal permeability increasing protein product - to  
 FT neutralise anticoagulant effect of heparin, to inhibit angiogenesis or  
 FT cell proliferation, as contraceptive and to reduce inflammation.  
 XX  
 PS Disclosure; Page 43-45; 78pp; English.  
 XX  
 CC This sequence represents the N-terminal of recombinant bactericidal/  
 CC permeability (rBPI) protein. This expression product encoding the 31  
 CC residue signal protein and the first 199 amino acids of the N-terminal of  
 CC mature human BPI has a molecular weight of 23 kD and is designated rBPI-  
 CC 23. In binding assays rBPI-23 was shown to have three separate functional  
 CC domains with heparin-binding activity, at least three major domains with  
 CC significant limulus amoebocyte lysate (LAL) inhibition and one region  
 CC with bactericidal activity. BPI, or active fragments of it may be used to  
 CC treat and prevent the effects of chronic inflammatory disease states such  
 CC as arthritis, psoriasis, inflammatory bowel disease, Crohn's disease and  
 CC asthma. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-  
 CC 2003 to correct PI field.)  
 XX SQ Sequence 487 AA;  
 Query Match 100.0%; Score 2507; DB 2; Length 487;  
 Best Local Similarity 100.0%; Pred No. 4.3e-229;  
 Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRENNARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRIISQKGLDYASQQTAAQLKEL 60  
 DB 1 MRENNARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRIISQKGLDYASQQTAAQLKEL 60  
 QY 61 KRIKIPYSDSFKIKHKGHYFSYMDIRFOLPSSQISMVNPNVGLKFSISNANIKISG 120  
 DB 61 KRIKIPYSDSFKIKHKGHYFSYMDIRFOLPSSQISMVNPNVGLKFSISNANIKISG 120  
 QY 121 KWKAQKFLKMSGNFSLIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180  
 DB 121 KWKAQKFLKMSGNFSLIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180  
 QY 181 KVGWLIQLFHKKIESALRNKNSQVCEKVTNSVSKLPQYFOTLPVMTKIDS VAGINYL 240  
 DB 181 KVGWLIQLFHKKIESALRNKNSQVCEKVTNSVSKLPQYFOTLPVMTKIDS VAGINYL 240  
 QY 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEPPAAHDMVYLGLSDYFFNTAGLV 300  
 DB 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEPPAAHDMVYLGLSDYFFNTAGLV 300  
 QY 301 YQEAGVLKMTLRDDMI PKESKFRLLTTFKFGTFLPEVAKKFNPMKIQIHVSASTPPHLSVQ 360  
 DB 301 YQEAGVLKMTLRDDMI PKESKFRLLTTFKFGTFLPEVAKKFNPMKIQIHVSASTPPHLSVQ 360  
 QY 361 PTGLTFFPAVDVQAFVLPNSLSASLFLIGHMTTGSMEVSAESNRLVGLKLDRLLELK 420  
 DB 361 PTGLTFFPAVDVQAFVLPNSLSASLFLIGHMTTGSMEVSAESNRLVGLKLDRLLELK 420  
 QY 421 HSNIGPPFVELLQDIMNVIIVLPVPRVNEKLGKGFPLTPARVOLXNVVLQPHONFLF 480  
 DB 421 HSNIGPPFVELLQDIMNVIIVLPVPRVNEKLGKGFPLTPARVOLXNVVLQPHONFLF 480  
 QY 481 GADVYK 487  
 DB 481 GADVYK 487

```

RESULT 4
AAR57901
ID AAR57901 standard; protein; 487 AA.
XX
XX AAR57901;
XX
XX 25-MAR-2003 (revised)
XX 29-MAR-1995 (first entry)
XX
XX Bactericide BPI.
XX
XX BPI; bactericidal-permeability-increasing protein; bactericide;
XX fusion protein; Gram-negative bacterium; infection.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1. .31
XX FT /label= Sig_peptide
XX
XX WO9418323-A1.
XX
XX 18-AUG-1994.
XX
XX 02-FEB-1994; 94WO-US001235.
XX
XX 02-FEB-1993; 93US-00013801.
XX
XX (XOMA ) XOMA CORP.
XX
XX Theofan G, Horwitz A, Burke D, Baltaian M, Grinna L;
XX
XX WPI; 1994-279744/34.
XX N-PSDB; AAQ67270.
XX
XX Bactericidal-permeability-increasing protein analogues with Cys132 or
XX Cys135 replaced - also fusion proteins and C-terminally truncated forms,
XX have increased stability and are useful to treat gram-negative bacterial
XX infection.
XX
XX Disclosure; Page 52-54; 77pp; English.
XX
XX Analogs, fusion proteins and C-terminal truncated forms of human BPI are
XX claimed that show improved resistance to dimerization and adduct
XX formation. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 487 AA;
XX
Query Match 100.0%; Score 2507; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPVGVVVRISQKGLDYASQGGTAALQKEL 60
Db 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPVGVVVRISQKGLDYASQGGTAALQKEL 60
Qy 61 KRKIPDYSDFKIKHLGKGHSYFSDIREFQLPSSQISNVPNVLKFSISNANIKISG 120
Db 61 KRKIPDYSDFKIKHLGKGHSYFSDIREFQLPSSQISNVPNVLKFSISNANIKISG 120
Qy 121 KWKAQKFLKWSGNFDLSIEGMSISADLKLSNPTSGKPTITCSCSSHNSVHVHLSKS 180
Db 121 KWKAQKFLKWSGNFDLSIEGMSISADLKLSNPTSGKPTITCSCSSHNSVHVHLSKS 180
Qy 181 KVGWLIQLFHKKIBSALRNKNSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240
Db 181 KVGWLIQLFHKKIBSALRNKNSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240
Qy 241 VAPPATTAETLDVQMKGEFSENHNPPPPAPPVMEFFPAADRMYVLGLSDYFNTAGLV 300
Db 241 VAPPATTAETLDVQMKGEFSENHNPPPPAPPVMEFFPAADRMYVLGLSDYFNTAGLV 300

301 YQEAGVLKMTLRDDMIPKESKFLRTTKFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
301 YQEAGVLKMTLRDDMIPKESKFLRTTKFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
361 PTGLTFYPADVQAFVLPNSSIASLFLIGMHTTGSMEVSAESNRLVGBELKDRLLLELK 420
361 PTGLTFYPADVQAFVLPNSSIASLFLIGMHTTGSMEVSAESNRLVGBELKDRLLLELK 420
421 HSNIGPFPVELLDIMNYIVPILVLPVNEKLGKQGLPPTPARVOLYNNVVLQPHQNFLLF 480
421 HSNIGPFPVELLDIMNYIVPILVLPVNEKLGKQGLPPTPARVOLYNNVVLQPHQNFLLF 480
481 GADVVK 487
481 GADVVK 487

RESULT 5
AAR62344
ID AAR62344 standard; protein; 487 AA.
XX
XX AAR62344;
XX
XX 25-MAR-2003 (revised)
XX 02-MAY-1995 (first entry)
XX
XX Recombinant 23 kD human BPI N-terminal protein.
XX
XX BPI; bactericidal/permeability-increasing protein; rBPI23; therapy;
XX treatment; infection; Mycobacteria; leprosy; tuberculosis; LAM;
XX lipoarabinomannan; improved pulmonary clearance; gram negative;
XX pneumonia model.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1. .31
XX FT /label= signal_sequence
XX Protein 32. 487
XX FT /label= N-terminus_of_human_BPI_holo protein
XX
XX WO9420129-A1.
XX
XX 15-SEP-1994.
XX
XX 11-MAR-1994; 94WO-US002463.
XX
XX 12-MAR-1993; 93US-00031145.
XX
XX (XOMA ) XOMA CORP.
XX
XX Lambert LH;
XX
XX WPI; 1994-302680/37.
XX N-PSDB; AAQ72017.
XX
XX Treating Mycobacterium infections with bactericidal-permeability inducing
XX peptide - also used for in vivo and in vitro neutralisation of
XX mycobacterial liparabinomannan.
XX
XX Disclosure; Page 21-23; 35pp; English.
XX
XX AAR62344 shows the recombinant 23 kD, 199 amino acid residue amino-
XX terminal fragment of human BPI (bactericidal/permeability-increasing
XX protein) holoprotein referred to as rBPI23. The sequence given is taken
XX from Grey et al., and varies to that from Gazzano-Santoro et al. In the
XX latter, the valine at position 141 is specified by GTG rather than GTC
XX and residue 185 is glutamic acid (specified by GAG) rather than lysine
XX (specified by AAG). The expression vector also encodes for a 31 residue
XX signal sequence. rBPI23 or biologically active deriva. are useful in the
XX treating of a subject suffering from any of the physiological effects of
XX LAM (lipoarabinomannan) from Mycobacteria. (Updated on 25-MAR-2003 to
XX correct PN field.)

```

XX SQ Sequence 487 AA;

Query Match 100.0%; Score 2507; DB 2; Length 487;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-229; Mismatches 0; Indels 0; Gaps 0;  
 Matches 487; Conservative 0;

Qy 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQOQTAAALQKEL 60  
 Db 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQOQTAAALQKEL 60

Qy 61 KRIKIPYSDSFKIKHLGKGHYFSYMDIREFQLPSSQISWPNVGLKFSISNANIKISG 120  
 Db 61 KRIKIPYSDSFKIKHLGKGHYFSYMDIREFQLPSSQISWPNVGLKFSISNANIKISG 120

Qy 121 KWKAQKFLKMGNGFDLSIEGMSISADLKLSNPTSGKPTITCSSSHINSVHVHISKS 180  
 Db 121 KWKAQKFLKMGNGFDLSIEGMSISADLKLSNPTSGKPTITCSSSHINSVHVHISKS 180

Qy 181 KVGWLIQLFHKKIESALRNKNQSVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240  
 Db 181 KVGWLIQLFHKKIESALRNKNQSVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240

Qy 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAAHDMVYLGSDYFFNTAGLV 300  
 Db 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAAHDMVYLGSDYFFNTAGLV 300

Qy 301 YQEAGVLKMTLRDDMI PKESKFRLTTFKFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360  
 Db 301 YQEAGVLKMTLRDDMI PKESKFRLTTFKFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360

Qy 361 PTGLTTFYPAVDVQAFVLPNSSLASFLIGHHTTGSMEVSAESNRLVGELKLDRLLELK 420  
 Db 361 PTGLTTFYPAVDVQAFVLPNSSLASFLIGHHTTGSMEVSAESNRLVGELKLDRLLELK 420

Qy 421 HSNIGPPPEVLLQDIMNVIPIVLPRVNEKLGKGFPLPTPARVOLYNNVLOPHQNFLLF 480  
 Db 421 HSNIGPPPEVLLQDIMNVIPIVLPRVNEKLGKGFPLPTPARVOLYNNVLOPHQNFLLF 480

Qy 481 GADVYK 487  
 Db 481 GADVYK 487

## RESULT 6

AAR68923  
 ID AAR68923 standard; protein; 487 AA.

XX AC AAR68923;

XX DT 25-MAR-2003 (revised)  
 XX DT 11-SEP-1995 (first entry)

XX DE Bactericidal/permeability-increasing protein (rBPI).

XX KW Lipopolysaccharide binding protein; rLPS; LPS; BPI;  
 XX KW gram-negative bacterial infections; treatment;  
 XX KW bactericidal/permeability-increasing protein.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 XX FT Peptide 1..32  
 XX FT /label= sig\_peptide

XX FN W09500641-A1.

XX PD 05-JAN-1995.

XX PF 17-JUN-1994; 94WO-US006931.

XX PR 17-JUN-1993; 93US-00079510.

XX XX

PA (XOMA ) XOMA CORP.

XX PI Gazzano-Santoro H, Theofan G, Trown PW;

XX DR WPI; 1995-052078/07.

XX DR N-PSDB; AAQ80827.

XX PT binding protein deriv. and hybrid protein binds to lipo:polysaccharide -  
 PT lacks CD14-mediated immuno-stimulatory properties, used to treat Gram-  
 negative bacterial infections and associated conditions.

XX PS Example 2; Page 70-72; 11app; English.

XX CC AAQ80827 encodes AAR68923 recombinant bactericidal/permeability-  
 CC increasing protein (rBPI). The protein contains the lipopolysaccharide  
 CC (LPS) binding domain fragments described in AAR68919-R68921. The  
 CC fragments are used in the construction of hybrid proteins for the  
 CC treatment gram-negative bacterial infections and associated conditions.  
 CC (Updated on 25-MAR-2003 to correct FN field.)

XX SQ Sequence 487 AA;

Query Match 100.0%; Score 2507; DB 2; Length 487;

Best Local Similarity 100.0%; Pred. No. 4.3e-229; Mismatches 0; Indels 0; Gaps 0;  
 Matches 487; Conservative 0;

Qy 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQOQTAAALQKEL 60

Db 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQOQTAAALQKEL 60

Qy 61 KRIKIPYSDSFKIKHLGKGHYFSYMDIREFQLPSSQISWPNVGLKFSISNANIKISG 120

Db 61 KRIKIPYSDSFKIKHLGKGHYFSYMDIREFQLPSSQISWPNVGLKFSISNANIKISG 120

Qy 121 KWKAQKFLKMGNGFDLSIEGMSISADLKLSNPTSGKPTITCSSSHINSVHVHISKS 180

Db 121 KWKAQKFLKMGNGFDLSIEGMSISADLKLSNPTSGKPTITCSSSHINSVHVHISKS 180

Qy 181 KVGWLIQLFHKKIESALRNKNQSVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240

Db 181 KVGWLIQLFHKKIESALRNKNQSVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240

Qy 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAAHDMVYLGSDYFFNTAGLV 300

Db 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAAHDMVYLGSDYFFNTAGLV 300

Qy 301 YQEAGVLKMTLRDDMI PKESKFRLTTFKFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360

Db 301 YQEAGVLKMTLRDDMI PKESKFRLTTFKFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360

Qy 361 PTGLTTFYPAVDVQAFVLPNSSLASFLIGHHTTGSMEVSAESNRLVGELKLDRLLELK 420

Db 361 PTGLTTFYPAVDVQAFVLPNSSLASFLIGHHTTGSMEVSAESNRLVGELKLDRLLELK 420

Qy 421 HSNIGPPPEVLLQDIMNVIPIVLPRVNEKLGKGFPLPTPARVOLYNNVLOPHQNFLLF 480

Db 421 HSNIGPPPEVLLQDIMNVIPIVLPRVNEKLGKGFPLPTPARVOLYNNVLOPHQNFLLF 480

Qy 481 GADVYK 487

Db 481 GADVYK 487

## RESULT 7

AAR79185  
 ID AAR79185 standard; protein; 487 AA.

XX AC AAR79185;

XX DT 25-MAR-2003 (revised)

XX DT 21-DEC-1995 (first entry)

XX DE Recombinant bactericidal/permeability-increasing protein rBPI.

```

XX Bactericidal/permeability-increasing protein; BPI; endotoxin;
KW Gram negative bacteria.
XX
XX Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..31
FT /label= signal
PN WO9519784-A1.
XX
XX 27-JUL-1995.
XX
XX 24-JAN-1995; 95WO-US0001151.
XX
XX 24-JAN-1994; 94US-00188221.
PR 16-AUG-1994; 94US-00291112.
XX
XX (XOMA ) XOMA CORP.
PA
XX Friedmann N, Scannon PJ, Van Deventer SJH, Von Der Mohlen MAM;
PI Wedel N;
XX
XX WPI; 1995-269271/35.
DR N-PSDB; AAQ97483.
XX
XX Treatment of humans exposed to bacterial endotoxin in circulation - using
PT bactericidal/permeability-increasing protein product to alleviate
PT increase in circulating tumour necrosis factor and interleukin 6.
XX
XX Disclosure; Page 43-45; 68pp; English.
XX
XX Bactericidal/permeability-increasing protein (BPI) is a protein extracted
CC from the granules of mammalian polymorphonuclear neutrophils. The mol.
CC wt. of the entire human BPI protein is approx. 55,000 daltons. The AA
CC sequence of the entire human BPI protein, as well as the DNA encoding the
CC protein, have been elucidated in Figure 1 of Gray et al., J. Biol. Chem.
CC 264:9505 (1989) and are incorporated by reference. In Gazzano-Santoro et
CC al., Infect. Immun. 60:4754-4761 (1992) an expression vector was used as
CC a source of DNA encoding a recombinant expression product (rBPI23) having
CC the 31- residue signal sequence and the first 199 AAs of the N-terminus
CC of the mature human BPI, as set out in Figure 1 of Gray et al., except
CC that Val151 is specified by GTG rather than GTC, and residue 185 is Glu
CC (specified by GAG) rather than Lys (specified by AAG). Recombinant
CC holoprotein (rBPI) has also been produced having the sequence
CC (AAQ97483/R79185) set out in Figure 1 of Gray et al., with the exceptions
CC noted for rBPI23 and the exception that residue 417 is Ala (specified
CC by GCT) rather than Val (specified by GTT). In the spec., the BPI protein
CC product is used for the treatment of humans exposed to bacterial
CC endotoxin in circulation. BPI protein products are administered in dosage
CC ants. of 0.1-10 mg/kg body wt. by parenteral routes. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
XX Sequence 487 AA;
SQ
Query Match 100.0%; Score 2507; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRSQKGLDYASQQGTAALQKEL 60
DB 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRSQKGLDYASQQGTAALQKEL 60
QY 61 KRIKIPDYSDFKIKHLGKHGHSFYSDMDIREFQLPSSQISWPNVGLKFSISNANIKISG 120
DB 61 KRIKIPDYSDFKIKHLGKHGHSFYSDMDIREFQLPSSQISWPNVGLKFSISNANIKISG 120
QY 121 KWKAKRQKFLKQSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180
DB 121 KWKAKRQKFLKQSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180
QY 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLQPVFQTLPVMTKIDSVAGINYGL 240

```

```

DB 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLQPVFQTLPVMTKIDSVAGINYGL 240
QY 241 VAPPATTAAETLDVQMKGEFYSENHNHPPFPAPPVMEFPAAHDRMVYLGSLSDYFFNTAGLV 300
DB 241 VAPPATTAAETLDVQMKGEFYSENHNHPPFPAPPVMEFPAAHDRMVYLGSLSDYFFNTAGLV 300
QY 301 YQEAGVLKMTLRDDMIPIKESKPRLTTKFTGTFLPEVAKKFPNNMKIQIHVSASTPPHLSVQ 360
DB 301 YQEAGVLKMTLRDDMIPIKESKPRLTTKFTGTFLPEVAKKFPNNMKIQIHVSASTPPHLSVQ 360
QY 361 PTGLTFYPADVQAFVAVLPNSLASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELX 420
DB 361 PTGLTFYPADVQAFVAVLPNSLASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELX 420
QY 421 HSNIGFPVELLQDINNYIVPILVLPVNEKLOKGFPLPTPARVQLYNNVVLQPHQNFLLF 480
DB 421 HSNIGFPVELLQDINNYIVPILVLPVNEKLOKGFPLPTPARVQLYNNVVLQPHQNFLLF 480
QY 481 GADVYK 487
DB 481 GADVYK 487
XX
XX RESULT 8
XX AAR79021
XX ID AAR79021 standard; protein; 487 AA.
XX
XX AAR79021;
XX
XX 25-MAR-2003 (revised)
DT 25-JAN-1996 (first entry)
XX
XX Bactericidal/permeability increasing protein.
XX
XX Bactericidal permeability increasing protein; BPI; infection; control;
KW recombinant.
XX
XX Homo sapiens.
OS
XX US5439807-A.
PN
XX 08-AUG-1995.
PD
XX 19-MAY-1993; 93US-00072063.
PF
XX 19-MAY-1992; 92US-00885501.
PR
XX (XOMA ) XOMA CORP.
PA
XX Grinna LS;
PI
XX WPI; 1995-283094/37.
DR N-PSDB; AAQ97607.
XX
XX Recovery of recombinant endotoxin binding protein - by culturing
PT transformed cells in medium contg. cation exchange material, useful for
PT treatment of bacterial infections.
XX
XX Example 1; Col 13-16; 18pp; English.
PS
XX Recombinant endotoxin-binding protein comprising bactericidal/
CC permeability increasing protein (BPI) or its endotoxin N-terminal
CC fragment, can be produced by growing genetically transformed host cells
CC in a suitable medium so that BPI is secreted into the medium. The BPI
CC is then isolated and can be used to control bacterial infections.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 487 AA;
SQ
Query Match 100.0%; Score 2507; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```



```

QY 1 MRENMARGPCNAPRWVSLMVLVAIGTAVTAAVNGVGVVRIISQKGLDYASQOQTAALQKEL 60
DB 1 MRENMARGPCNAPRWVSLMVLVAIGTAVTAAVNGVGVVRIISQKGLDYASQOQTAALQKEL 60

QY 61 KRIKIPDYSDSPFKIKHLKGHYSPYMDIREPQLPSSQISWPNVGLKFSINANIKISG 120
DB 61 KRIKIPDYSDSPFKIKHLKGHYSPYMDIREPQLPSSQISWPNVGLKFSINANIKISG 120

QY 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180
DB 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180

QY 181 KVGWLIQLFHHKIESALRNKMSQVCEKVTNSVSKLQPFQTLPMVKIDSVAGINYL 240
DB 181 KVGWLIQLFHHKIESALRNKMSQVCEKVTNSVSKLQPFQTLPMVKIDSVAGINYL 240

QY 241 VAPPATTATLTVQMGKGFYSYSENHNPPPPFAPVMEFPAADRMVYLGSDYFFNTAGLV 300
DB 241 VAPPATTATLTVQMGKGFYSYSENHNPPPPFAPVMEFPAADRMVYLGSDYFFNTAGLV 300

QY 301 YOEAGVLMKWLTRDDMI PKESKFRLLTKFPGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
DB 301 YOEAGVLMKWLTRDDMI PKESKFRLLTKFPGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360

QY 361 PTGLTFYPADVQAFVLPNSLSLFLIGMHTTGSMEVSASRNRLVGLKLDRLLELK 420
DB 361 PTGLTFYPADVQAFVLPNSLSLFLIGMHTTGSMEVSASRNRLVGLKLDRLLELK 420

QY 421 HSNIGPPFVELLDIMNVIPTLVLPVNEKLOKGFPLPTPARVQLYNNVLOPHQNFLLF 480
DB 421 HSNIGPPFVELLDIMNVIPTLVLPVNEKLOKGFPLPTPARVQLYNNVLOPHQNFLLF 480

QY 481 GADVYVK 487
DB 481 GADVYVK 487

RESULT 9
AAR81247
ID AAR81247 standard; protein; 487 AA.
XX AC AAR81247;
XX DT 18-MAR-1996 (first entry)
XX DE Recombinant bactericidal/permeability increasing holoprotein.
XX KW Bactericidal/permeability increasing protein; BPI; granule; mammalian;
KW polymorphonuclear neutrophil; anti-bacterial; fungus; infection; ss;
KW antifungal; fluconazole; amphotericin B; Candida albicans; sterilise;
KW lipopolysaccharide binding protein; protein; sterilisation; medical instrument.
XX OS Synthetic.
XX FH Key
XX FT Peptide
FT 1. .31 Location/Qualifiers
FT 32. .487 /note= "signal peptide"
FT /note= "mature peptide"
XX PN W09519179-A1.
XX PD 20-JUL-1995.
XX PF 13-JAN-1995; 95WO-US000498.
XX PR 14-JAN-1994; 94US-00183222.
XX PR 11-MAR-1994; 94US-00209762.
XX PR 11-JUL-1994; 94US-00273540.
XX PA (XOMA ) XOMA CORP.
XX

```

```

PI Little RG, Lim E, Scannon PJ, Lambert LH;
XX WPI; 1995-263713/34.
DR N-PSDB; AAQ99816.
XX
PT Treating fungal infection with bactericidal permeability increasing
PT protein or deriv. - esp. for control of systemic Candida albicans
PT infection or for use in in vitro sterilisation.
XX
PS Example 1; Page 105-107; 153pp; English.
XX
CC The amino acid sequence of a recombinant bactericidal/permeability
CC increasing (BPI) protein. BPI protein can be isolated from the granules
CC of mammalian polymorphonuclear neutrophils (PMN). The protein has
CC antibacterial activity associated with 3 functional domains: I
CC (AAR81085), II (AAR81086) and III (AAR81087) present in N-terminal region
CC of the BPI holoprotein (AAR81245). The antibacterial regions were used to
CC design the antifungal peptides AAR81083-4, AAR81088-R81244 and AAR81248-
CC R81308. The peptides are used to treat fungal infections together with
CC other antifungal cpds e.g. fluconazole or amphotericin B. The antifungal
CC activity of the peptides may also be enhanced by addition of a
CC lipopolysaccharide binding protein (LBP) e.g. AAR81246. The peptides can
CC be used to treat fungal infection, esp. Candida albicans. They are also
CC usefull for killing or inhibiting fungi in vitro e.g. for sterilising
CC medical instruments
XX
SQ Sequence 487 AA;
Query Match 100.0%; Score 2507; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRENMARGPCNAPRWVSLMVLVAIGTAVTAAVNGVGVVRIISQKGLDYASQOQTAALQKEL 60
DB 1 MRENMARGPCNAPRWVSLMVLVAIGTAVTAAVNGVGVVRIISQKGLDYASQOQTAALQKEL 60

QY 61 KRIKIPDYSDSPFKIKHLKGHYSPYMDIREPQLPSSQISWPNVGLKFSINANIKISG 120
DB 61 KRIKIPDYSDSPFKIKHLKGHYSPYMDIREPQLPSSQISWPNVGLKFSINANIKISG 120

QY 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180
DB 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180

QY 181 KVGWLIQLFHHKIESALRNKMSQVCEKVTNSVSKLQPFQTLPMVKIDSVAGINYL 240
DB 181 KVGWLIQLFHHKIESALRNKMSQVCEKVTNSVSKLQPFQTLPMVKIDSVAGINYL 240

QY 241 VAPPATTATLTVQMGKGFYSYSENHNPPPPFAPVMEFPAADRMVYLGSDYFFNTAGLV 300
DB 241 VAPPATTATLTVQMGKGFYSYSENHNPPPPFAPVMEFPAADRMVYLGSDYFFNTAGLV 300

QY 301 YOEAGVLMKWLTRDDMI PKESKFRLLTKFPGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
DB 301 YOEAGVLMKWLTRDDMI PKESKFRLLTKFPGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360

QY 361 PTGLTFYPADVQAFVLPNSLSLFLIGMHTTGSMEVSASRNRLVGLKLDRLLELK 420
DB 361 PTGLTFYPADVQAFVLPNSLSLFLIGMHTTGSMEVSASRNRLVGLKLDRLLELK 420

QY 421 HSNIGPPFVELLDIMNVIPTLVLPVNEKLOKGFPLPTPARVQLYNNVLOPHQNFLLF 480
DB 421 HSNIGPPFVELLDIMNVIPTLVLPVNEKLOKGFPLPTPARVQLYNNVLOPHQNFLLF 480

QY 481 GADVYVK 487
DB 481 GADVYVK 487

RESULT 10
AAR80995
ID AAR80995 standard; protein; 487 AA.
XX

```

```
AC AAR80995;
XX
XX DT 23-MAY-1996 (first entry)
XX
XX DE Bactericidal/permeability increasing protein (rBPI).
XX
XX KW bactericidal/permeability increasing peptide; BPI; heparin; binding;
XX neutralisation; lipopolysaccharide; LPS; bactericidal activity;
XX treatment; neutralise endotoxin; inhibit angiogenesis;
XX inhibit tumour formation; proliferation.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX Peptide 1..31
XX Protein /label= Signal_peptide
XX /label= mature_peptide
XX
XX W09519372-A1.
XX
XX PD 20-JUL-1995.
XX
XX PF 15-SEP-1994; 94WO-US010427.
XX
XX PR 14-JAN-1994; 94US-00183222.
XX
XX PR 11-MAR-1994; 94US-00209762.
XX
XX PA (XOMA ) XOMA CORP.
XX
XX PI Little RG;
XX
XX DR WPI; 1995-263828/34.
XX
XX DR N-PSDB; AAT00951.
XX
XX PT New peptide(s) based on bactericidal/permeability-increasing protein -
XX having heparin binding and neutralisation, LPS binding and neutralisation
XX and antimicrobial activities.
XX
XX PS Disclosure; Page 147-150; 275pp; English.
XX
XX CC Recombinant bactericidal/permeability increasing protein (rBPI) is
XX encoded by AAT00951. BPI (bactericidal permeability-increasing) peptides
XX (AAR80996-81081 and AAR82553-372) each have an amino acid sequence that
XX is deriv. of a BPI functional domain (or a variant) having at least one
XX of the biological activities of BPI, such as heparin binding or
XX neutralisation; lipopolysaccharide (LPS) binding or neutralisation or
XX bactericidal activity. The BPI peptides are based on the amino-terminal
XX portion of BPI, esp. functional domains I, II, and III (BPI residues 17-
XX 45, 65-99 and 142-169 resp.)
XX
XX SQ Sequence 487 AA;
XX
XX Query Match 100.0%; Score 2507; DB 2; Length 487;
XX Best Local Similarity 100.0%; Pred. No. 4.3e-229;
XX Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANVGVVVRISQKGLDYASQGGTAALQKEL 60
XX DB 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANVGVVVRISQKGLDYASQGGTAALQKEL 60
XX
XX QY 61 KRIKIPDYSDFKIKHLGKGHSYSDMDIREFQIPSSQISMPVNVGLKFSISNANIKISG 120
XX DB 61 KRIKIPDYSDFKIKHLGKGHSYSDMDIREFQIPSSQISMPVNVNVGLKFSISNANIKISG 120
XX
XX QY 121 KWKAQKRLKMGNFDSLIEGMSISADLKAGSNPTSGKPTITCSSSHINSVHVHISKS 180
XX DB 121 KWKAQKRLKMGNFDSLIEGMSISADLKAGSNPTSGKPTITCSSSHINSVHVHISKS 180
XX
XX QY 181 KVGWLIQLFHHKIKIESALRNKNQSVCEKVTNSVSKLPYFQTLPLVMTKIDSVAGINYL 240
XX DB 181 KVGWLIQLFHHKIKIESALRNKNQSVCEKVTNSVSKLPYFQTLPLVMTKIDSVAGINYL 240
```

```
QY 241 VAPPATTAETLDVQMKGEFYSENHNPPPPFAPPVMEFPAAHDMRVYLGLSDFYFNTAGLV 300
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 241 VAPPATTAETLDVQMKGEFYSENHNPPPPFAPPVMEFPAAHDMRVYLGLSDFYFNTAGLV 300
QY 301 YQEAGVLKMTLRDDMI PKESKFLRTTKFCTFLPEVAKKFPNNMKIQIHVSASTPPHLSVQ 360
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 301 YQEAGVLKMTLRDDMI PKESKFLRTTKFCTFLPEVAKKFPNNMKIQIHVSASTPPHLSVQ 360
QY 361 PTGLTTPYPAVDVQAFPAVLNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELK 420
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 361 PTGLTTPYPAVDVQAFPAVLNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELK 420
QY 421 HSNIGPFPVELLQDINNYIVPILVLRVNEKLGKGFPLPTPARVQLYNVVLQPHQNFLLF 480
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 421 HSNIGPFPVELLQDINNYIVPILVLRVNEKLGKGFPLPTPARVQLYNVVLQPHQNFLLF 480
QY 481 GADVVK 487
DB |||||||
DB 481 GADVVK 487

RESULT 11
AAR67998
ID AAR67998 standard; protein; 487 AA.
XX
XX AC AAR67998;
XX
XX DT 25-MAR-2003 (revised)
XX DT 15-AUG-1995 (first entry)
XX
XX DE Hologrotein rBPI50.
XX
XX KW Bactericidal/permeability-increasing protein; BPI; rBPI; rBPI50;
XX lipopolysaccharide binding protein; LBP; rLBP25; rLBP;
XX Gram-negative bacterium; infection; antiseptic.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX Peptide 1..31
XX /label= Sig_peptide
XX Peptide 32..487
XX /label= Mat_peptide
XX /note= "rBPI50 holoprotein"
XX
XX PN W09502414-A1.
XX
XX PD 26-JAN-1995.
XX
XX PF 13-JUL-1994; 94WO-US007834.
XX
XX PR 14-JUL-1993; 93US-00093201.
XX PR 11-JUL-1994; 94US-00274303.
XX
XX PA (XOMA ) XOMA CORP.
XX
XX PI Horwitz A;
XX
XX DR WPI; 1995-067161/09.
XX DR N-PSDB; AAQ81445.
XX
XX PT Method for treating gram negative bacterial infection - comprises
XX administering lipopolysaccharide binding protein (LBP) prod. and
XX bactericidal/permeability-increasing (BPI) protein prod.
XX
XX PS Disclosure; Page 36-38; 76pp; English.
XX
XX CC Gram-negative bacterial infections are treated by co-administration of
XX BPI protein and LBP. Recombinant BPI 50 kda holoprotein rBPI50 (given in
XX AAR67998) is the preferred BPI. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX
XX SQ Sequence 487 AA;
```

Query Match	100.0%; Score 2507; DB 2; Length 487;	
Best Local Similarity	100.0%; Pred. No. 4.3e-229;	
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDVASQOGTAALQKEL 60	
DB	1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDVASQOGTAALQKEL 60	
QY	61 KRKIPIYSDSPFKIHLGKGHSFYSDIRFQLPSSQISWPNVGLKFSISNANIKISG 120	
DB	61 KRKIPIYSDSPFKIHLGKGHSFYSDIRFQLPSSQISWPNVGLKFSISNANIKISG 120	
QY	121 KWAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTTTCSSCSHINSVHVHISKS 180	
DB	121 KWAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTTTCSSCSHINSVHVHISKS 180	
QY	181 KVGWLIQLFHKHIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240	
DB	181 KVGWLIQLFHKHIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240	
QY	241 VAPPATTAETLDVQMGGEFYSENHNHPPFPAPVMEFFPAAHDMVYLGSLDYFFNTAGLV 300	
DB	241 VAPPATTAETLDVQMGGEFYSENHNHPPFPAPVMEFFPAAHDMVYLGSLDYFFNTAGLV 300	
QY	301 YQEAGVLKMTLRDDMI PKESKFLRTTKFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360	
DB	301 YQEAGVLKMTLRDDMI PKESKFLRTTKFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360	
QY	361 PTGLTFYPADVQAFVLPNSLSIASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420	
DB	361 PTGLTFYPADVQAFVLPNSLSIASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420	
QY	421 HSNIGPFPVELLDQIMNYIVPILVLRVNEKLGKGFPLTPARVOLYNVVLQPHQNFLLF 480	
DB	421 HSNIGPFPVELLDQIMNYIVPILVLRVNEKLGKGFPLTPARVOLYNVVLQPHQNFLLF 480	
QY	481 GADVYK 487	
DB	481 GADVYK 487	
RESULT 12		
AAR86455		
ID	AAR86455 standard; protein; 487 AA.	
XX		
AC	AAR86455;	
XX		
DT	15-MAR-1996 (first entry)	
XX		
DE	rBPI for use in treating liver damage.	
XX		
KW	BPI; bactericidal permeability increasing protein; RES;	
KW	reticuloendothelial; Kupffer cells; liver insult; hepatotoxic;	
KW	hepatectomy; trauma; viral hepatitis; chronic inflammatory.	
XX		
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	Protein	32..487
FT		/label= rBPI
XX		
PN	WO9510297-A1.	
XX		
PD	20-APR-1995.	
XX		
PF	05-OCT-1994; 94WO-US011404.	
XX		
PR	15-OCT-1993; 93US-00132510.	
XX		
PA	(XOMA ) XOMA CORP.	
XX		
PI	Van Leeuwen PA, Boormeester MA;	



CC	2003 to correct PF field.)	
XX	Sequence 487 AA;	
SQ	Query Match	
	Best Local Similarity 100.0%; Score 2507; DB 2; Length 487;	
	Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MRENMGPCNAPRWVSLMVLVAIGTAVTAANPGVGVVIRISQKGLDYASQQTAAALQKEL 60	
DB	1 MRENMGPCNAPRWVSLMVLVAIGTAVTAANPGVGVVIRISQKGLDYASQQTAAALQKEL 60	
QY	61 KRIKIPDYSDFKIKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISG 120	
DB	61 KRIKIPDYSDFKIKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISG 120	
QY	121 KWAQKRFKMGSGNFDLSIEGMSISADLKLSNPTSGKPTITCSCSSHINSVHVHISKS 180	
DB	121 KWAQKRFKMGSGNFDLSIEGMSISADLKLSNPTSGKPTITCSCSSHINSVHVHISKS 180	
QY	181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLOPYFQTLPMVKIDS VAGINYL 240	
DB	181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLOPYFQTLPMVKIDS VAGINYL 240	
QY	241 VAPPATTAAETLDVQMKGEFYSNHNPPFPAPVMEFFAAHDMVYLGSLDYFFNTAGLV 300	
DB	241 VAPPATTAAETLDVQMKGEFYSNHNPPFPAPVMEFFAAHDMVYLGSLDYFFNTAGLV 300	
QY	301 YOEAGVLKMTLRDDMIPEKSKFRLTKPGTFLPEVAKKFPNMKQIHVSASTPPHLSVQ 360	
DB	301 YOEAGVLKMTLRDDMIPEKSKFRLTKPGTFLPEVAKKFPNMKQIHVSASTPPHLSVQ 360	
QY	361 PTGLTFYPADVQAFVLPNSLSLFLIGMHTTGSMEVSAESNRLVGLKDLRLLELK 420	
DB	361 PTGLTFYPADVQAFVLPNSLSLFLIGMHTTGSMEVSAESNRLVGLKDLRLLELK 420	
QY	421 HSNIGPPFVELLDIMNVIPIVLPRVNEKLOKGFPLPTPARVOLYNNVLOPHQNFLIF 480	
DB	421 HSNIGPPFVELLDIMNVIPIVLPRVNEKLOKGFPLPTPARVOLYNNVLOPHQNFLIF 480	
QY	481 GADVYK 487	
DB	481 GADVYK 487	
RESULT 15		
AAR97568		
ID	AAR97568 standard; protein; 487 AA.	
XX		
AC	AAR97568;	
XX		
DT	25-FEB-1997 (first entry)	
XX		
DE	Human bactericidal permeability increasing protein.	
XX		
KW	rBPI; recombinant; bactericidal permeability increasing protein;	
KW	anti-microbial; polyoxypropylene-polyoxyethylene block copolymer;	
KW	poloxamer; surfactant; inhibition; antibiotic.	
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..31
FT		/label= signal
FT	Protein	32..487
FT		/label= rBPI
XX		
PN	WO9621436-A1.	
XX		
PD	18-JUL-1996.	
XX		
PF	16-JAN-1996; 96WO-US001095.	
XX		

Search completed: October 21, 2005, 11:26:46  
Job time : 174.559 secs

PR	13-JAN-1995; 95US-00372104.	
PR	19-SEP-1995; 95US-00530599.	
XX	(XOMA ) XOMA CORP.	
PA	Lambert LH;	
XX	WPI; 1996-342029/34.	
DR	N-PSDB; AAT31853.	
XX	Compen. comprising bactericidal permeability increasing protein prod. and	
PT	bactericidal activity enhancing poloxamer surfactant - useful for	
PT	treating bacterial infections, and for inhibiting bacterial and fungal	
PT	growth.	
XX	Claim 1; Page 75-76; 83pp; English.	
XX	The known anti-microbial properties of bactericidal/permeability	
CC	increasing protein (BPI) can be enhanced by administering the BPI with a	
CC	stabilising polyoxypropylene-polyoxyethylene block copolymer (poloxamer).	
CC	Therapeutic compositions pref. contain one of the poloxamers 333, 334,	
CC	335 or 403 and opt. comprise EDTA. They are useful for treating bacterial	
CC	and fungal infections. The present sequence is that of human recombinant	
CC	BPI and was disclosed in Gray et al., J.Biol.Chem., 264:9505 (1989)	
XX		
SQ	Sequence 487 AA;	
	Query Match	
	Best Local Similarity 100.0%; Score 2507; DB 2; Length 487;	
	Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MRENMGPCNAPRWVSLMVLVAIGTAVTAANPGVGVVIRISQKGLDYASQQTAAALQKEL 60	
DB	1 MRENMGPCNAPRWVSLMVLVAIGTAVTAANPGVGVVIRISQKGLDYASQQTAAALQKEL 60	
QY	61 KRIKIPDYSDFKIKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISG 120	
DB	61 KRIKIPDYSDFKIKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISG 120	
QY	121 KWAQKRFKMGSGNFDLSIEGMSISADLKLSNPTSGKPTITCSCSSHINSVHVHISKS 180	
DB	121 KWAQKRFKMGSGNFDLSIEGMSISADLKLSNPTSGKPTITCSCSSHINSVHVHISKS 180	
QY	181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLOPYFQTLPMVKIDS VAGINYL 240	
DB	181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLOPYFQTLPMVKIDS VAGINYL 240	
QY	241 VAPPATTAAETLDVQMKGEFYSNHNPPFPAPVMEFFAAHDMVYLGSLDYFFNTAGLV 300	
DB	241 VAPPATTAAETLDVQMKGEFYSNHNPPFPAPVMEFFAAHDMVYLGSLDYFFNTAGLV 300	
QY	301 YOEAGVLKMTLRDDMIPEKSKFRLTKPGTFLPEVAKKFPNMKQIHVSASTPPHLSVQ 360	
DB	301 YOEAGVLKMTLRDDMIPEKSKFRLTKPGTFLPEVAKKFPNMKQIHVSASTPPHLSVQ 360	
QY	361 PTGLTFYPADVQAFVLPNSLSLFLIGMHTTGSMEVSAESNRLVGLKDLRLLELK 420	
DB	361 PTGLTFYPADVQAFVLPNSLSLFLIGMHTTGSMEVSAESNRLVGLKDLRLLELK 420	
QY	421 HSNIGPPFVELLDIMNVIPIVLPRVNEKLOKGFPLPTPARVOLYNNVLOPHQNFLIF 480	
DB	421 HSNIGPPFVELLDIMNVIPIVLPRVNEKLOKGFPLPTPARVOLYNNVLOPHQNFLIF 480	
QY	481 GADVYK 487	
DB	481 GADVYK 487	

This Page Blank (uspto)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2005, 11:22:45 ; Search time 64.7154 Seconds  
(without alignments)  
1187.019 Million cell updates/sec

Title: US-10-629-516-2\_COPY\_10\_193  
Perfect score: 943  
Sequence: 1 CNAPRWSLMVLVAIGTAVT.....HVHISKVKGWGLQLFHKKI 184

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09D\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US10F\_PUBCOMB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US10G\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	943	100.0	483	10	US-09-759-130B-408
2	943	100.0	483	13	US-10-042-431-38
3	943	100.0	483	16	US-10-741-790-408
4	943	100.0	483	16	US-10-473-127-1170
5	943	100.0	483	16	US-10-473-127-1170
6	943	100.0	487	9	US-09-765-527-265
7	943	100.0	487	9	US-09-760-397-16
8	943	100.0	487	9	US-09-881-490-206
9	943	100.0	487	9	US-09-942-021-2
10	943	100.0	487	9	US-09-733-613-2
11	943	100.0	487	9	US-09-728-938-2
					Sequence 408, App
					Sequence 38, Appl
					Sequence 408, App
					Sequence 1170, Ap
					Sequence 1241, Ap
					Sequence 265, App
					Sequence 16, Appl
					Sequence 206, App
					Sequence 2, Appl
					Sequence 2, Appl

12	943	100.0	487	9	US-09-782-642-2	Sequence 2, Appli
13	943	100.0	487	9	US-09-255-245-2	Sequence 2, Appli
14	943	100.0	487	9	US-09-941-198A-2	Sequence 2, Appli
15	943	100.0	487	9	US-09-866-514-2	Sequence 2, Appli
16	943	100.0	487	9	US-09-861-400-4	Sequence 4, Appli
17	943	100.0	487	9	US-09-861-400-15	Sequence 15, Appli
18	943	100.0	487	10	US-09-746-311-2	Sequence 2, Appli
19	943	100.0	487	10	US-09-975-638B-3	Sequence 3, Appli
20	943	100.0	487	10	US-09-416-828-2	Sequence 2, Appli
21	943	100.0	487	10	US-09-480-234-2	Sequence 2, Appli
22	943	100.0	487	13	US-10-006-517-2	Sequence 2, Appli
23	943	100.0	487	14	US-10-226-810-2	Sequence 2, Appli
24	943	100.0	487	14	US-10-128-139-2	Sequence 2, Appli
25	943	100.0	487	14	US-10-196-460-2	Sequence 2, Appli
26	943	100.0	487	14	US-10-146-136-2	Sequence 2, Appli
27	943	100.0	487	14	US-10-209-621-28	Sequence 28, Appli
28	943	100.0	487	14	US-10-131-686A-12	Sequence 12, Appli
29	943	100.0	487	14	US-10-324-182-16	Sequence 16, Appli
30	943	100.0	487	15	US-10-404-724-2	Sequence 2, Appli
31	943	100.0	487	15	US-10-342-169A-2	Sequence 2, Appli
32	943	100.0	487	15	US-10-299-985-2	Sequence 2, Appli
33	943	100.0	487	15	US-10-162-743-2	Sequence 2, Appli
34	943	100.0	487	15	US-10-446-628-69	Sequence 69, Appli
35	943	100.0	487	15	US-10-446-628-146	Sequence 146, App
36	943	100.0	487	15	US-10-319-786-69	Sequence 69, Appli
37	943	100.0	487	15	US-10-359-013-13	Sequence 13, Appli
38	943	100.0	487	16	US-10-716-389-2	Sequence 2, Appli
39	943	100.0	487	16	US-10-473-127-1151	Sequence 1151, Ap
40	943	100.0	487	16	US-10-473-127-1152	Sequence 1152, Ap
41	943	100.0	487	16	US-10-473-127-1153	Sequence 1153, Ap
42	943	100.0	487	16	US-10-473-127-1154	Sequence 1154, Ap
43	943	100.0	487	16	US-10-473-127-1155	Sequence 1155, Ap
44	943	100.0	487	16	US-10-473-127-1156	Sequence 1156, Ap
45	943	100.0	487	16	US-10-473-127-1157	Sequence 1157, Ap

ALIGNMENTS

RESULT 1  
US-09-759-130B-408  
; Sequence 408, Application US/09759130B  
; Publication No. US2003002279A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: McCarthy, Sean A  
; APPLICANT: Fraser, Christopher C  
; APPLICANT: Sharp, John D  
; APPLICANT: Barnes, Thomas S  
; APPLICANT: Kirt, Susan J  
; APPLICANT: Mackay, Charles R  
; APPLICANT: Myers, Paul S  
; APPLICANT: Leiby, Kevin R  
; APPLICANT: Wrighton, Nicolas  
; APPLICANT: Goodearl, Andrew  
; APPLICANT: Holtzman, Douglas A  
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE,  
; TITLE OF INVENTION: USES  
; FILE REFERENCE: MP100-5350WNIM  
; CURRENT APPLICATION NUMBER: US/09/759,130B  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: US 09/479,249  
; PRIOR FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: US 09/559,497  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 09/578,063  
; PRIOR FILING DATE: 2000-05-24  
; PRIOR APPLICATION NUMBER: US 09/333,159  
; PRIOR FILING DATE: 1999-06-14  
; PRIOR APPLICATION NUMBER: US 09/596,194  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 09/342,364

THERAPEUTIC, AND OTHER

```

; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 408
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-759-1308-408

Query Match      100.0%; Score 943; DB 10; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.4e-84;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 60
    |||||
Db 6 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 65

QY 61 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKQKRF 120
    |||||
Db 66 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKQKRF 125

QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTTCSSCSHINSVHVHISKSKVGLIQLF 180
    |||||
Db 126 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTTCSSCSHINSVHVHISKSKVGLIQLF 185

QY 181 HKKI 184
    |||||
Db 186 HKKI 189

RESULT 3
US-10-741-790-408
; Sequence 408, Application US/10741790
; Publication No. US20040121396A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirt, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: MPI00-5350NNIM
; CURRENT APPLICATION NUMBER: US/10/741,790
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 408
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-741-790-408

Query Match      100.0%; Score 943; DB 16; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.4e-84;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 60
    |||||
Db 6 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 65

QY 61 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKQKRF 120
    |||||

```



Db 66 DSFKIKHLKGHYSFYSMDIREFQLPSSQISNVPVNLKFSISNANIKISGKWAQKRF 125  
 Qy 121 KMSGNFDLSIEGMSISADLKLSNPTSGKPTITCSCSSHNSVHVHISKSVGWLQ 180  
 Db 126 KMSGNFDLSIEGMSISADLKLSNPTSGKPTITCSCSSHNSVHVHISKSVGWLQ 185  
 Qy 181 HKKI 184  
 Db 186 HKKI 189

RESULT 4

US-10-473-127-1170  
 ; Sequence 1170, Application US/10473127  
 ; Publication No. US20040236091A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zycos Inc.  
 ; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
 ; FILE REFERENCE: 08191-026W01  
 ; CURRENT APPLICATION NUMBER: US/10/473,127  
 ; CURRENT FILING DATE: 2003-09-26  
 ; PRIOR APPLICATION NUMBER: 60/279,495  
 ; PRIOR FILING DATE: 2001-03-28  
 ; PRIOR APPLICATION NUMBER: 60/292,544  
 ; PRIOR FILING DATE: 2001-05-21  
 ; PRIOR APPLICATION NUMBER: 60/310,801  
 ; PRIOR FILING DATE: 2001-08-08  
 ; PRIOR APPLICATION NUMBER: 60/326,370  
 ; PRIOR FILING DATE: 2001-10-01  
 ; PRIOR APPLICATION NUMBER: 60/336,780  
 ; PRIOR FILING DATE: 2001-12-04  
 ; PRIOR APPLICATION NUMBER: 60/358,985  
 ; PRIOR FILING DATE: 2002-02-20  
 ; NUMBER OF SEQ ID NOS: 2041  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1170  
 ; LENGTH: 483  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-473-127-1170

Query Match 100.0%; Score 943; DB 16; Length 483;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-84;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CNAPRWVSLMVLVAIGTAVTAANPVGVVVRSQKGLDYASOQGTAAQKELKRIKIPDYS 60  
 Db 6 CNAPRWVSLMVLVAIGTAVTAANPVGVVVRSQKGLDYASOQGTAAQKELKRIKIPDYS 65  
 Qy 61 DSFKIKHLKGHYSFYSMDIREFQLPSSQISNVPVNLKFSISNANIKISGKWAQKRF 120  
 Db 66 DSFKIKHLKGHYSFYSMDIREFQLPSSQISNVPVNLKFSISNANIKISGKWAQKRF 125  
 Qy 121 KMSGNFDLSIEGMSISADLKLSNPTSGKPTITCSCSSHNSVHVHISKSVGWLQ 180  
 Db 126 KMSGNFDLSIEGMSISADLKLSNPTSGKPTITCSCSSHNSVHVHISKSVGWLQ 185  
 Qy 181 HKKI 184  
 Db 186 HKKI 189

RESULT 5

US-10-473-127-1241  
 ; Sequence 1241, Application US/10473127  
 ; Publication No. US20040236091A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zycos Inc.  
 ; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
 ; FILE REFERENCE: 08191-026W01  
 ; CURRENT APPLICATION NUMBER: US/10/473,127  
 ; CURRENT FILING DATE: 2003-09-26  
 ; PRIOR APPLICATION NUMBER: 60/279,495

; PRIOR FILING DATE: 2001-03-28  
 ; PRIOR APPLICATION NUMBER: 60/292,544  
 ; PRIOR FILING DATE: 2001-05-21  
 ; PRIOR APPLICATION NUMBER: 60/310,801  
 ; PRIOR FILING DATE: 2001-08-08  
 ; PRIOR APPLICATION NUMBER: 60/326,370  
 ; PRIOR FILING DATE: 2001-10-01  
 ; PRIOR APPLICATION NUMBER: 60/336,780  
 ; PRIOR FILING DATE: 2001-12-04  
 ; PRIOR APPLICATION NUMBER: 60/358,985  
 ; PRIOR FILING DATE: 2002-02-20  
 ; NUMBER OF SEQ ID NOS: 2041  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1241  
 ; LENGTH: 483  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-473-127-1241

Query Match 100.0%; Score 943; DB 16; Length 483;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-84;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CNAPRWVSLMVLVAIGTAVTAANPVGVVVRSQKGLDYASOQGTAAQKELKRIKIPDYS 60  
 Db 6 CNAPRWVSLMVLVAIGTAVTAANPVGVVVRSQKGLDYASOQGTAAQKELKRIKIPDYS 65  
 Qy 61 DSFKIKHLKGHYSFYSMDIREFQLPSSQISNVPVNLKFSISNANIKISGKWAQKRF 120  
 Db 66 DSFKIKHLKGHYSFYSMDIREFQLPSSQISNVPVNLKFSISNANIKISGKWAQKRF 125  
 Qy 121 KMSGNFDLSIEGMSISADLKLSNPTSGKPTITCSCSSHNSVHVHISKSVGWLQ 180  
 Db 126 KMSGNFDLSIEGMSISADLKLSNPTSGKPTITCSCSSHNSVHVHISKSVGWLQ 185  
 Qy 181 HKKI 184  
 Db 186 HKKI 189

RESULT 6

US-09-765-527-265  
 ; Sequence 265, Application US/09765527  
 ; Patent No. US20020006638A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Better, Marc D.  
 ; TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
 ; Fusion Proteins and BPI-Derived Peptides  
 ; NUMBER OF SEQUENCES: 265  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: United States of America  
 ; ZIP: 60606-6402  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION NUMBER: US/09/765,527  
 ; FILING DATE: 18-Jan-2001  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/621,803  
 ; FILING DATE: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Borun, Michael F.  
 ; REGISTRATION NUMBER: 25,447  
 ; REFERENCE/DOCKET NUMBER: 27129/33199  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 265:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 265:  
US-09-765-527-265  
Query Match 100.0%; Score 943; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 3.5e-84;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQTAALQKELKRIKIPDYS 60  
Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQTAALQKELKRIKIPDYS 69  
Qy 61 DSKFKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKRFL 120  
Db 70 DSKFKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKRFL 129  
Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKSKVGLIQLF 180  
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKSKVGLIQLF 189  
Qy 181 HKKI 184  
Db 190 HKKI 193

RESULT 7  
US-09-760-397-16  
Sequence 16, Application US/09760397  
Patent No. US2002009781A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Gavitt, Patrick D.  
TITLE OF INVENTION: Improved Methods for Recombinant Peptide Production  
FILE REFERENCE: 1103/11041US01  
CURRENT APPLICATION NUMBER: US/09/760,397  
CURRENT FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: 09/271,970  
PRIOR FILING DATE: 1999-03-18  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 16  
LENGTH: 487  
TYPE: PRT  
ORGANISM: Human  
US-09-760-397-16  
Query Match 100.0%; Score 943; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 3.5e-84;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQTAALQKELKRIKIPDYS 60  
Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQTAALQKELKRIKIPDYS 69  
Qy 61 DSKFKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKRFL 120  
Db 70 DSKFKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKRFL 129  
Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKSKVGLIQLF 180  
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKSKVGLIQLF 189  
Qy 181 HKKI 184  
Db 190 HKKI 193

RESULT 8  
US-09-881-490-206  
Sequence 206, Application US/09881490  
Patent No. US20020077298A1  
GENERAL INFORMATION:  
APPLICANT: Little II, Roger G.  
Lim, Edward  
Fadem Mitchell B.  
TITLE OF INVENTION: Anti-Fungal Peptides  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th FloorDrive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/881,490  
FILING DATE: 14-Jun-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/119,858  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/372,105  
FILING DATE: 13-JAN-95  
APPLICATION NUMBER: 08/306,473  
FILING DATE: 15-SEP-94  
APPLICATION NUMBER: 08/273,540  
FILING DATE: 11-JUL-94  
APPLICATION NUMBER: 08/209,762  
FILING DATE: 11-MAR-94  
APPLICATION NUMBER: 08/183,222  
FILING DATE: 14-JAN-94  
APPLICATION NUMBER: 08/093,202  
FILING DATE: 15-JUL-93  
APPLICATION NUMBER: 08/030,644  
FILING DATE: 12-MAR-93  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 100-238/11021US01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 206:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 206:  
US-09-881-490-206  
Query Match 100.0%; Score 943; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 3.5e-84;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQTAALQKELKRIKIPDYS 60  
Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQTAALQKELKRIKIPDYS 69  
Qy 61 DSKFKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKRFL 120  
Db 70 DSKFKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKRFL 129  
Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKSKVGLIQLF 180

TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 265:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 265:  
US-09-765-527-265  
Query Match 100.0%; Score 943; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 3.5e-84;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQTAALQKELKRIKIPDYS 60  
Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQTAALQKELKRIKIPDYS 69  
Qy 61 DSKFKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKRFL 120  
Db 70 DSKFKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKRFL 129  
Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKSKVGLIQLF 180  
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKSKVGLIQLF 189  
Qy 181 HKKI 184  
Db 190 HKKI 193

TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 265:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 265:  
US-09-765-527-265  
Query Match 100.0%; Score 943; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 3.5e-84;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQTAALQKELKRIKIPDYS 60  
Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQTAALQKELKRIKIPDYS 69  
Qy 61 DSKFKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKRFL 120  
Db 70 DSKFKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKRFL 129  
Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKSKVGLIQLF 180

Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTICSSSSHINSVHVHISKVGVWLIQLF 189  
Qy 181 HKKI 184  
Db 190 HKKI 193

RESULT 9  
US-09-942-021-2  
; Sequence 2, Application US/09942021  
; Patent No. US20020090368A1  
; GENERAL INFORMATION:  
; APPLICANT: Little, Roger G. II  
; TITLE OF INVENTION: Therapeutic Uses of Bactericidal/Permeability  
; Increasing (BPI) Protein Products  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 W. Madison Street, 34th Floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/942,021  
; FILING DATE: 27-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/220,427  
; FILING DATE: 24-DEC-1998  
; APPLICATION NUMBER: 08/415,158  
; FILING DATE: March 31, 1995  
; APPLICATION NUMBER: 08/093,202  
; FILING DATE: July 15, 1993  
; APPLICATION NUMBER: 08/030,644  
; FILING DATE: March 12, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11004US07 / 100-224.P1.C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 487 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-942-021-2

Query Match 100.0%; Score 943; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 3.5e-84;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 60  
Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 69  
Qy 61 DSFKIKHLKGHYSFYSDMIREFQLPSSQISWVPNVGLKFSISNANIKISGKWKAKQKRF 120  
Db 70 DSFKIKHLKGHYSFYSDMIREFQLPSSQISWVPNVGLKFSISNANIKISGKWKAKQKRF 129  
Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTICSSSSHINSVHVHISKVGVWLIQLF 180  
Db 122 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTICSSSSHINSVHVHISKVGVWLIQLF 189

Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTICSSSSHINSVHVHISKVGVWLIQLF 189  
Qy 181 HKKI 184  
Db 190 HKKI 193  
RESULT 10  
US-09-733-613-2  
; Sequence 2, Application US/09733613  
; Patent No. US20020094952A1  
; GENERAL INFORMATION:  
; APPLICANT: Friedmann, Nadav  
; Scannon, Patrick J.  
; van Deventer, Sander J.H.  
; von der Mohlen, Marijke A.M.  
; Wedel, Nancy  
; TITLE OF INVENTION: Human Therapeutic Uses of BPI Protein Products  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/733,613  
; FILING DATE: 08-Dec-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/388,758  
; FILING DATE: 1999-09-02  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michael F. Borun  
; REGISTRATION NUMBER: 25,447  
; REFERENCE/DOCKET NUMBER: 27129/32451  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 487 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-733-613-2

Query Match 100.0%; Score 943; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 3.5e-84;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 60  
Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 69  
Qy 61 DSFKIKHLKGHYSFYSDMIREFQLPSSQISWVPNVGLKFSISNANIKISGKWKAKQKRF 120  
Db 70 DSFKIKHLKGHYSFYSDMIREFQLPSSQISWVPNVGLKFSISNANIKISGKWKAKQKRF 129  
Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTICSSSSHINSVHVHISKVGVWLIQLF 180  
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTICSSSSHINSVHVHISKVGVWLIQLF 189  
Qy 181 HKKI 184

D**b** 190 HKKI 193

RESULT 11

```

US-09-728-938-2
: Sequence 2, Application US/09728938
: Patent No. US20020103114A1
: GENERAL INFORMATION:
: APPLICANT: Giroir, Brett P.
:           Shannon, Patrick J.
: TITLE OF INVENTION: Therapeutic Uses of BPI Protein Products
:           for Human Meningococcemia
:
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/728,938
: FILING DATE: 30-Dec-2000
: CLASSIFICATION: <Unknown>
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/365,858
: FILING DATE: <Unknown>
: APPLICATION NUMBER: 08/927,437
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Sharp, Jeffrey S.
: REGISTRATION NUMBER: 31,879
: REFERENCE/DOCKET NUMBER: 27129/33248
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEX: 25-3856
:
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 487 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-728-938-2

```

```

US-09-782-642-2
; Sequence 2, Application US/09782642
; Patent No. US20020103118A1
; GENERAL INFORMATION:
; APPLICANT: Lewis H. Lambert, Jr.
; TITLE OF INVENTION: Treatment of Mycobacterial Diseases
; by Administration of
; Bactericidal/Permeability-Increasing
; Protein Product
;
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,642
; FILING DATE: 13-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/626,646
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31293
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-782-642-2

```

RESULT 13  
US-09-255-245-2  
; Sequence 2, Application US/09255245  
; Patent No. US20020119918A1  
; GENERAL INFORMATION:

```

; APPLICANT: Cartoll, Stephen F.
; TITLE OF INVENTION: THERAPEUTIC USES OF N-TERMINAL BPI PROTEIN
; TITLE OF INVENTION: PRODUCTS IN ANCA-POSITIVE PATIENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/255,245
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/742,985
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/33565
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-255-245-2

Query Match 100.0%; Score 943; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 3.5e-84;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNAPRWSLMVLVAIGTAVTAANPGVVRISQKGLDYASQGTAAALQKELKRIKIPDYS 60
DB 10 CNAPRWSLMVLVAIGTAVTAANPGVVRISQKGLDYASQGTAAALQKELKRIKIPDYS 69
QY 61 DSFKIKHLGKHGHSFYSDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFL 120
DB 70 DSFKIKHLGKHGHSFYSDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFL 129
QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSHINSVHVHISKSKVGWLIQLF 180
DB 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSHINSVHVHISKSKVGWLIQLF 189
QY 181 HKKI 184
DB 190 HKKI 193

RESULT 14
US-09-941-198A-2
; Sequence 2, Application US/09941198A
; Patent No. US2002012819A1
; GENERAL INFORMATION:
; APPLICANT: Scannon, Patrick J.
; TITLE OF INVENTION: METHODS OF TREATING CONDITIONS
; ASSOCIATED WITH CORNEAL INJURY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Borun

```

```

; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/941,198A
; FILING DATE: 27-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/557,289
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-941-198A-2

Query Match 100.0%; Score 943; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 3.5e-84;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNAPRWSLMVLVAIGTAVTAANPGVVRISQKGLDYASQGTAAALQKELKRIKIPDYS 60
DB 10 CNAPRWSLMVLVAIGTAVTAANPGVVRISQKGLDYASQGTAAALQKELKRIKIPDYS 69
QY 61 DSFKIKHLGKHGHSFYSDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFL 120
DB 70 DSFKIKHLGKHGHSFYSDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFL 129
QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSHINSVHVHISKSKVGWLIQLF 180
DB 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSHINSVHVHISKSKVGWLIQLF 189
QY 181 HKKI 184
DB 190 HKKI 193

RESULT 15
US-09-866-514-2
; Sequence 2, Application US/09866514
; Patent No. US20020137050A1
; GENERAL INFORMATION:
; APPLICANT: Elsbach and Weiss
; TITLE OF INVENTION: THERAPEUTIC USES OF BACTERICIDAL/PERMEABILITY-INCREASING
; PROTEIN FRAGMENTS
; FILE REFERENCE: 28297/32248B
; CURRENT APPLICATION NUMBER: US/09/866,514
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 09/309,217
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 487
; TYPE: PRT

```

```
; ORGANISM: Homo sapiens
US-09-866-514-2
Query Match      100.0%; Score 943; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 3.5e-84;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CNAPRWVSLMVLVAIGTAVTAAYNPVGWVVRISQKGLDYASQQGTAALQKELKEIKIPDYS 60
Db      10 CNAPRWVSLMVLVAIGTAVTAAYNPVGWVVRISQKGLDYASQQGTAALQKELKEIKIPDYS 69
Qy      61 DPFKIKHLGKHGHSFYSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKQKRF 120
Db      70 DPFKIKHLGKHGHSFYSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKQKRF 129
Qy      121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKSKVGWLIQLF 180
Db      130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKSKVGWLIQLF 189
Qy      181 HKKI 184
Db      190 HKKI 193
```

Search completed: October 21, 2005, 11:37:02  
Job time : 65.7154 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2005, 11:22:45 ; Search time 171.285 Seconds  
(without alignments)  
1187.019 Million cell updates/sec

Title: US-10-629-516-2  
Perfect score: 2507  
Sequence: 1 MRENARGPCNAPRWVSLMV.....NVVLQHQNFLFGADVVK 487

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues  
Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : Published Applications AA:\*

1:	/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2:	/cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6:	/cgn2_6/ptodata/1/pubpaa/PTCTUS_PUBCOMB.pep.*
7:	/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8:	/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9:	/cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10:	/cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11:	/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12:	/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13:	/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14:	/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15:	/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16:	/cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17:	/cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18:	/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19:	/cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20:	/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2507	100.0	487	9	US-09-765-527-265
2	2507	100.0	487	9	US-09-760-397-16
3	2507	100.0	487	9	US-09-881-490-206
4	2507	100.0	487	9	US-09-942-021-2
5	2507	100.0	487	9	US-09-733-613-2
6	2507	100.0	487	9	US-09-728-938-2
7	2507	100.0	487	9	US-09-782-642-2
8	2507	100.0	487	9	US-09-255-245-2
9	2507	100.0	487	9	US-09-941-198A-2
10	2507	100.0	487	9	US-09-866-514-2
11	2507	100.0	487	9	US-09-861-400-15
					Sequence 265, App
					Sequence 16, Appl
					Sequence 206, App
					Sequence 2, Appl
					Sequence 2, Appl
					Sequence 2, Appl
					Sequence 2, Appl
					Sequence 2, Appl
					Sequence 2, Appl
					Sequence 2, Appl
					Sequence 2, Appl
					Sequence 15, Appl

12	2507	100.0	487	10	US-09-746-311-2
13	2507	100.0	487	10	US-09-975-638B-3
14	2507	100.0	487	10	US-09-416-828-2
15	2507	100.0	487	10	US-09-480-234-2
16	2507	100.0	487	13	US-10-006-557-2
17	2507	100.0	487	14	US-10-226-810-2
18	2507	100.0	487	14	US-10-128-139-2
19	2507	100.0	487	14	US-10-196-460-2
20	2507	100.0	487	14	US-10-146-136-2
21	2507	100.0	487	14	US-10-209-621-28
22	2507	100.0	487	14	US-10-131-686A-12
23	2507	100.0	487	14	US-10-324-182-16
24	2507	100.0	487	15	US-10-404-724-2
25	2507	100.0	487	15	US-10-342-169A-2
26	2507	100.0	487	15	US-10-299-985-2
27	2507	100.0	487	15	US-10-162-743-2
28	2507	100.0	487	15	US-10-446-628-69
29	2507	100.0	487	15	US-10-446-628-146
30	2507	100.0	487	15	US-10-319-786-69
31	2507	100.0	487	15	US-10-359-013-13
32	2507	100.0	487	16	US-10-716-389-2
33	2507	100.0	487	16	US-10-473-127-1151
34	2507	100.0	487	16	US-10-473-127-1152
35	2507	100.0	487	16	US-10-473-127-1153
36	2507	100.0	487	16	US-10-473-127-1154
37	2507	100.0	487	16	US-10-473-127-1155
38	2507	100.0	487	16	US-10-473-127-1156
39	2507	100.0	487	16	US-10-473-127-1157
40	2507	100.0	487	16	US-10-473-127-1158
41	2507	100.0	487	16	US-10-473-127-1159
42	2507	100.0	487	16	US-10-473-127-1160
43	2507	100.0	487	16	US-10-473-127-1161
44	2507	100.0	487	16	US-10-473-127-1162
45	2507	100.0	487	16	US-10-473-127-1163

ALIGNMENTS

RESULT 1  
US-09-765-527-265  
; Sequence 265, Application US/09765527  
; Patent No. US20020006638A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides  
; NUMBER OF SEQUENCES: 265  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/765,527  
; FILING DATE: 18-Jan-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/621,803  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Borun, Michael F.  
; REGISTRATION NUMBER: 25,447  
; REFERENCE/DOCKET NUMBER: 27129/33199  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448





FILING DATE: 11-JUL-94  
APPLICATION NUMBER: 08/209,762  
FILING DATE: 11-MAR-94  
APPLICATION NUMBER: 08/183,222  
FILING DATE: 14-JAN-94  
APPLICATION NUMBER: 08/093,202  
FILING DATE: 15-JUL-93  
APPLICATION NUMBER: 08/030,644  
FILING DATE: 12-MAR-93  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 100-238/11021US01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 206:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 206:  
US-09-881-490-206

Query Match 100.0%; Score 2507; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 1.7e-209; Indels 0; Gaps 0;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAAVNPVGVVRIISQKGLDYASQQGTAALQKEL 60  
DB 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAAVNPVGVVRIISQKGLDYASQQGTAALQKEL 60  
QY 61 KRIKIPDYSDFKIKHLKGHYSFYSDMIREFQLPSSQISWPNVGLKFSINANIKISG 120  
DB 61 KRIKIPDYSDFKIKHLKGHYSFYSDMIREFQLPSSQISWPNVGLKFSINANIKISG 120  
QY 121 KWKAKRFLKMSGNFDSLIEGMSISADLKGNSPTSGKPTITCSSCSHINSVHVHISKS 180  
DB 121 KWKAKRFLKMSGNFDSLIEGMSISADLKGNSPTSGKPTITCSSCSHINSVHVHISKS 180  
QY 181 KVGWLIQLFHKKIESALRNKNMSQCEKVTNSVSSKLPQYFQTLPMVTKIDS VAGINYL 240  
DB 181 KVGWLIQLFHKKIESALRNKNMSQCEKVTNSVSSKLPQYFQTLPMVTKIDS VAGINYL 240  
QY 241 VAPPATTATLTVQMKGEFYSENHNPPFPAPVMEFFPAADRMVYLGSLDYFFNTAGLV 300  
DB 241 VAPPATTATLTVQMKGEFYSENHNPPFPAPVMEFFPAADRMVYLGSLDYFFNTAGLV 300  
QY 301 YOEAGVLKMTLRDDMI PKESKRLTTKFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQ 360  
DB 301 YOEAGVLKMTLRDDMI PKESKRLTTKFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQ 360  
QY 361 PTGLTFYPADVQFAVLPNSLASLFLTGHTTGSMEVSAESNRLVGLKLDRLLELK 420  
DB 361 PTGLTFYPADVQFAVLPNSLASLFLTGHTTGSMEVSAESNRLVGLKLDRLLELK 420  
QY 421 HSNIGFPVELLDQIMNYIVPILVLPVNEKLOKGFPLTPARVOLYNNVLOPHONFLIF 480  
DB 421 HSNIGFPVELLDQIMNYIVPILVLPVNEKLOKGFPLTPARVOLYNNVLOPHONFLIF 480  
QY 481 GADVYK 487  
DB 481 GADVYK 487

RESULT 4  
US-09-942-021-2  
Sequence 2, Application US/09942021  
Patent No. US20020090368A1  
GENERAL INFORMATION:  
APPLICANT: Little, Roger G. II

TITLE OF INVENTION: Therapeutic Uses of Bactericidal/Permeability  
Increasing (BPI) Protein Products  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 W. Madison Street, 34th Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/942,021  
FILING DATE: 27-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/220,427  
FILING DATE: 24-DEC-1998  
APPLICATION NUMBER: 08/415,158  
FILING DATE: March 31, 1995  
APPLICATION NUMBER: 08/093,202  
FILING DATE: July 15, 1993  
APPLICATION NUMBER: 08/030,644  
FILING DATE: March 12, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11004US07 / 100-224.P1.C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-942-021-2

Query Match 100.0%; Score 2507; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 1.7e-209; Indels 0; Gaps 0;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAAVNPVGVVRIISQKGLDYASQQGTAALQKEL 60  
DB 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAAVNPVGVVRIISQKGLDYASQQGTAALQKEL 60  
QY 61 KRIKIPDYSDFKIKHLKGHYSFYSDMIREFQLPSSQISWPNVGLKFSINANIKISG 120  
DB 61 KRIKIPDYSDFKIKHLKGHYSFYSDMIREFQLPSSQISWPNVGLKFSINANIKISG 120  
QY 121 KWKAKRFLKMSGNFDSLIEGMSISADLKGNSPTSGKPTITCSSCSHINSVHVHISKS 180  
DB 121 KWKAKRFLKMSGNFDSLIEGMSISADLKGNSPTSGKPTITCSSCSHINSVHVHISKS 180  
QY 181 KVGWLIQLFHKKIESALRNKNMSQCEKVTNSVSSKLPQYFQTLPMVTKIDS VAGINYL 240  
DB 181 KVGWLIQLFHKKIESALRNKNMSQCEKVTNSVSSKLPQYFQTLPMVTKIDS VAGINYL 240  
QY 241 VAPPATTATLTVQMKGEFYSENHNPPFPAPVMEFFPAADRMVYLGSLDYFFNTAGLV 300  
DB 241 VAPPATTATLTVQMKGEFYSENHNPPFPAPVMEFFPAADRMVYLGSLDYFFNTAGLV 300  
QY 301 YOEAGVLKMTLRDDMI PKESKRLTTKFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQ 360  
DB 301 YOEAGVLKMTLRDDMI PKESKRLTTKFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQ 360

QY 361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420  
DB 361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420  
QY 421 HSNIGPPVELLDIMNYIVPILVPRVNEKLOKGFPLPTPARVQLYNVVVLQPHQNFLLF 480  
DB 421 HSNIGPPVELLDIMNYIVPILVPRVNEKLOKGFPLPTPARVQLYNVVVLQPHQNFLLF 480  
QY 481 GADVVK 487  
DB 481 GADVVK 487  
RESULT 5  
US-09-733-613-2  
; Sequence 2, Application US/09733613  
; Patent No. US20020094952A1  
; GENERAL INFORMATION:  
; APPLICANT: Friedmann, Nadav  
; Scannon, Patrick J.  
; van Deventer, Sander J.H.  
; von der Mohlen, Marijke A.M.  
; Wedel, Nancy  
; TITLE OF INVENTION: Human Therapeutic Uses of BPI Protein Products  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/733.613  
; FILING DATE: 08-Dec-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/388,758  
; FILING DATE: 1993-09-02  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michael F. Borun  
; REGISTRATION NUMBER: 25,447  
; REFERENCE/DOCKET NUMBER: 27129/32451  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 487 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-733-613-2  
Query Match 100.0%; Score 2507; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 1.7e-209;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRENWAGPCNAPRWVSLWLVALGTAVTAAVNPGVVVRSQKGLDYASQOGTAALQKEL 60  
DB 1 MRENWAGPCNAPRWVSLWLVALGTAVTAAVNPGVVVRSQKGLDYASQOGTAALQKEL 60  
QY 61 KRKIPDYSDFKIKHLKGHYSPYSDIREFQLPSSQIGMVPNVVGLKFSISNANIKISG 120  
DB 61 KRKIPDYSDFKIKHLKGHYSPYSDIREFQLPSSQIGMVPNVVGLKFSISNANIKISG 120

QY 121 KWKAKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKS 180  
DB 121 KWKAKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKS 180  
QY 181 KVGWLIQLPHKKIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPMWTKIDS VAGIN YGL 240  
DB 181 KVGWLIQLPHKKIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPMWTKIDS VAGIN YGL 240  
QY 241 VAPPATTATLDOVMKGEFYSNNHNPFPFAPVMEFFPAADHDMVYLGLSDYFFENTAGLV 300  
DB 241 VAPPATTATLDOVMKGEFYSNNHNPFPFAPVMEFFPAADHDMVYLGLSDYFFENTAGLV 300  
QY 301 YQAGVLMKTLRDDMI PKESKFLRTTKFFGTLPPEVAKKFPNMKIQIHVSASTPPHLSVQ 360  
DB 301 YQAGVLMKTLRDDMI PKESKFLRTTKFFGTLPPEVAKKFPNMKIQIHVSASTPPHLSVQ 360  
QY 361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420  
DB 361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420  
QY 421 HSNIGPPVELLDIMNYIVPILVPRVNEKLOKGFPLPTPARVQLYNVVVLQPHQNFLLF 480  
DB 421 HSNIGPPVELLDIMNYIVPILVPRVNEKLOKGFPLPTPARVQLYNVVVLQPHQNFLLF 480  
QY 481 GADVVK 487  
DB 481 GADVVK 487  
RESULT 6  
US-09-728-938-2  
; Sequence 2, Application US/09728938  
; Patent No. US20020103114A1  
; GENERAL INFORMATION:  
; APPLICANT: Giroir, Brett P.  
; Scannon, Patrick J.  
; TITLE OF INVENTION: Therapeutic Uses of BPI Protein Products  
; for Human Meningococemia  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/728,938  
; FILING DATE: 30-Dec-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/365,858  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/927,437  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sharp, Jeffrey S.  
; REGISTRATION NUMBER: 31,879  
; REFERENCE/DOCKET NUMBER: 27129/33248  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 487 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

```

; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-728-938-2

Query Match      100.0%; Score 2507; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.7e-209; Indels 0; Gaps 0;
Matches 487; Conservative 0; Mismatches 0;

Qy 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQTAALQKEL 60
Db 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQTAALQKEL 60

Qy 61 KRIKIPDYSDFKIKHLGKGHYSFYSDMIRFQLPSSQISMVNVGLKFSISNANIKISG 120
Db 61 KRIKIPDYSDFKIKHLGKGHYSFYSDMIRFQLPSSQISMVNVGLKFSISNANIKISG 120

Qy 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180
Db 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180

Qy 181 KVGWLIQLFHKKIESALRNKNSQVCEKVTNSVSSKLOPYQTLPVMTKIDSVAGINYL 240
Db 181 KVGWLIQLFHKKIESALRNKNSQVCEKVTNSVSSKLOPYQTLPVMTKIDSVAGINYL 240

Qy 241 VAPPATTAAETLDVQMGKFYSENHNPPPPAPPVMEFPAADRMVYLGLSDYFFNTAGLV 300
Db 241 VAPPATTAAETLDVQMGKFYSENHNPPPPAPPVMEFPAADRMVYLGLSDYFFNTAGLV 300

Qy 301 YQEAGVLKWTLRDDMI PKESKFRLLTKPGFTFLPEVAKKFNMKIQIHVSASTPPHLSVQ 360
Db 301 YQEAGVLKWTLRDDMI PKESKFRLLTKPGFTFLPEVAKKFNMKIQIHVSASTPPHLSVQ 360

Qy 361 PTGLTFYPADVQAFVLPNSSLASFLIGHMTTGSMEVSAESNRLVGELKLDRLLELK 420
Db 361 PTGLTFYPADVQAFVLPNSSLASFLIGHMTTGSMEVSAESNRLVGELKLDRLLELK 420

Qy 421 HSNIGPFFVELLDIMNVIPIVLPVPRNEKIQGFPLTPARVOLYNNVLOPHONFLLF 480
Db 421 HSNIGPFFVELLDIMNVIPIVLPVPRNEKIQGFPLTPARVOLYNNVLOPHONFLLF 480

Qy 481 GADVVYK 487
Db 481 GADVVYK 487

RESULT 7
US-09-782-642-2
; Sequence 2, Application US/09782642
; Patent No. US20020103118A1
; GENERAL INFORMATION:
; APPLICANT: Lewis H. Lambert, Jr.
; TITLE OF INVENTION: Treatment of Mycobacterial Diseases
; by Administration of
; Bactericidal/Permeability-Increasing
; Protein Product
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/782,642
; APPLICATION NUMBER: US/09/782,642
; FILING DATE: 13-Feb-2001
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/626,646
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31293
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-782-642-2

Query Match      100.0%; Score 2507; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.7e-209; Indels 0; Gaps 0;
Matches 487; Conservative 0; Mismatches 0;

Qy 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQTAALQKEL 60
Db 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQTAALQKEL 60

Qy 61 KRIKIPDYSDFKIKHLGKGHYSFYSDMIRFQLPSSQISMVNVGLKFSISNANIKISG 120
Db 61 KRIKIPDYSDFKIKHLGKGHYSFYSDMIRFQLPSSQISMVNVGLKFSISNANIKISG 120

Qy 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180
Db 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180

Qy 181 KVGWLIQLFHKKIESALRNKNSQVCEKVTNSVSSKLOPYQTLPVMTKIDSVAGINYL 240
Db 181 KVGWLIQLFHKKIESALRNKNSQVCEKVTNSVSSKLOPYQTLPVMTKIDSVAGINYL 240

Qy 241 VAPPATTAAETLDVQMGKFYSENHNPPPPAPPVMEFPAADRMVYLGLSDYFFNTAGLV 300
Db 241 VAPPATTAAETLDVQMGKFYSENHNPPPPAPPVMEFPAADRMVYLGLSDYFFNTAGLV 300

Qy 301 YQEAGVLKWTLRDDMI PKESKFRLLTKPGFTFLPEVAKKFNMKIQIHVSASTPPHLSVQ 360
Db 301 YQEAGVLKWTLRDDMI PKESKFRLLTKPGFTFLPEVAKKFNMKIQIHVSASTPPHLSVQ 360

Qy 361 PTGLTFYPADVQAFVLPNSSLASFLIGHMTTGSMEVSAESNRLVGELKLDRLLELK 420
Db 361 PTGLTFYPADVQAFVLPNSSLASFLIGHMTTGSMEVSAESNRLVGELKLDRLLELK 420

Qy 421 HSNIGPFFVELLDIMNVIPIVLPVPRNEKIQGFPLTPARVOLYNNVLOPHONFLLF 480
Db 421 HSNIGPFFVELLDIMNVIPIVLPVPRNEKIQGFPLTPARVOLYNNVLOPHONFLLF 480

Qy 481 GADVVYK 487
Db 481 GADVVYK 487

RESULT 8
US-09-255-245-2
; Sequence 2, Application US/09255245
; Patent No. US20020119918A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Stephen F.
; TITLE OF INVENTION: THERAPEUTIC USES OF N-TERMINAL BPI PROTEIN
; PRODUCTS IN ANCA-POSITIVE PATIENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
```

```

; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/742,985
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/33565
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-255-245-2

```

```

Query Match 100.0%; Score 2507; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.7e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWISLMLVLAIGTAVTAAVNPGVVVRISQKGLDYASOOGTAALQKEL 60
Db 1 MRENARGPCNAPRWISLMLVLAIGTAVTAAVNPGVVVRISQKGLDYASOOGTAALQKEL 60

Qy 61 KRKIPDYSDFKIKHLGKGHYSFYSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISG 120
Db 61 KRKIPDYSDFKIKHLGKGHYSFYSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISG 120

Qy 121 KWKAQKRFKLMKSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180
Db 121 KWKAQKRFKLMKSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180

Qy 181 KVGLWLIQLFHKKIESALRNKNSQVCEKVTNSVSKLQPYFQTLPVMTKIDSVAGINYL 240
Db 181 KVGLWLIQLFHKKIESALRNKNSQVCEKVTNSVSKLQPYFQTLPVMTKIDSVAGINYL 240

Qy 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAAHDMVYLGSDYFNTAGLV 300
Db 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAAHDMVYLGSDYFNTAGLV 300

Qy 301 YQEAGVLKMTLRDDMI PKESKFRITTKFPGFTFLPEVAKKFPNMKI QIHVSASTPPHLSVQ 360
Db 301 YQEAGVLKMTLRDDMI PKESKFRITTKFPGFTFLPEVAKKFPNMKI QIHVSASTPPHLSVQ 360

Qy 361 PTGLTTFYPAVDVQAFVLPNSSLASFLI GHHHTTGSMEVSAESNRLVGEKLDRLLELK 420
Db 361 PTGLTTFYPAVDVQAFVLPNSSLASFLI GHHHTTGSMEVSAESNRLVGEKLDRLLELK 420

Qy 421 HSNIGPFPVELLQDIMNVIVILVPRVNEKLGKGFPLTPARVOLNVVLQPHQNFLLF 480
Db 421 HSNIGPFPVELLQDIMNVIVILVPRVNEKLGKGFPLTPARVOLNVVLQPHQNFLLF 480

Qy 481 GADVYK 487
Db 481 GADVYK 487

```

```

RESULT 9
US-09-941-198A-2
; Sequence 2, Application US/09941198A
; Patent No. US20020128191A1
; GENERAL INFORMATION:
; APPLICANT: Scannon, Patrick J.
; TITLE OF INVENTION: METHODS OF TREATING CONDITIONS
; ASSOCIATED WITH CORNEAL INJURY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/941,198A
; FILING DATE: 27-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/557,289
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-941-198A-2

```

```

Query Match 100.0%; Score 2507; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.7e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWISLMLVLAIGTAVTAAVNPGVVVRISQKGLDYASOOGTAALQKEL 60
Db 1 MRENARGPCNAPRWISLMLVLAIGTAVTAAVNPGVVVRISQKGLDYASOOGTAALQKEL 60

Qy 61 KRKIPDYSDFKIKHLGKGHYSFYSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISG 120
Db 61 KRKIPDYSDFKIKHLGKGHYSFYSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISG 120

Qy 121 KWKAQKRFKLMKSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180
Db 121 KWKAQKRFKLMKSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180

Qy 181 KVGLWLIQLFHKKIESALRNKNSQVCEKVTNSVSKLQPYFQTLPVMTKIDSVAGINYL 240
Db 181 KVGLWLIQLFHKKIESALRNKNSQVCEKVTNSVSKLQPYFQTLPVMTKIDSVAGINYL 240

Qy 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAAHDMVYLGSDYFNTAGLV 300
Db 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAAHDMVYLGSDYFNTAGLV 300

Qy 301 YQEAGVLKMTLRDDMI PKESKFRITTKFPGFTFLPEVAKKFPNMKI QIHVSASTPPHLSVQ 360

```

Db 301 YQAGVLKQTLRDDMI PKESKRLTTKFFGTFLPEVAKFPNMKIQIHVSASTPPHLSVQ 360  
Qy 361 PTGLTFYPAVDVQAFVLPNSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELK 420  
Db 361 PTGLTFYPAVDVQAFVLPNSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELK 420  
Qy 421 HSNIGPPFVELLDIMNYIVIPILVLPVNEKLOKGFPLTPARVOLYNNVLOPHQNFLLF 480  
Db 421 HSNIGPPFVELLDIMNYIVIPILVLPVNEKLOKGFPLTPARVOLYNNVLOPHQNFLLF 480  
Qy 481 GADVYK 487  
Db 481 GADVYK 487

RESULT 10  
US-09-866-514-2  
; Sequence 2, Application US/09866514  
; Patent No. US20020137050A1  
; GENERAL INFORMATION:  
; APPLICANT: Elsbach and Weiss  
; TITLE OF INVENTION: THERAPEUTIC USES OF BACTERICIDAL/PERMEABILITY-INCREASING  
; FILE REFERENCE: 28297/32248B  
; CURRENT APPLICATION NUMBER: US/09/866,514  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 09/309,217  
; PRIOR FILING DATE: 1999-05-10  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 487  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-866-514-2

Query Match 100.0%; Score 2507; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 1.7e-209;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWVSLMVLVAICTAVTAANPGVVVRI SQKGLDYASQQTAAQKEL 60  
Db 1 MRENARGPCNAPRWVSLMVLVAICTAVTAANPGVVVRI SQKGLDYASQQTAAQKEL 60  
Qy 61 KRIKIPYSDSFKIKHLKGHSFYSDMIREFQLPSSQISMVPPNVGLKFSISNANIKISG 120  
Db 61 KRIKIPYSDSFKIKHLKGHSFYSDMIREFQLPSSQISMVPPNVGLKFSISNANIKISG 120  
Qy 121 KWKAKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTTTCSSCSSHINSVHVHISKS 180  
Db 121 KWKAKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTTTCSSCSSHINSVHVHISKS 180  
Qy 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSKLOPYFQTLPMVTKIDS VAGINYL 240  
Db 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSKLOPYFQTLPMVTKIDS VAGINYL 240  
Qy 241 VAPPATTATLTDVQMKGEFYSENHNPPPPFAPVPMVEFPAADHDMVYLGSLSDYFFNTAGLV 300  
Db 241 VAPPATTATLTDVQMKGEFYSENHNPPPPFAPVPMVEFPAADHDMVYLGSLSDYFFNTAGLV 300  
Qy 301 YQAGVLKQTLRDDMI PKESKRLTTKFFGTFLPEVAKFPNMKIQIHVSASTPPHLSVQ 360  
Db 301 YQAGVLKQTLRDDMI PKESKRLTTKFFGTFLPEVAKFPNMKIQIHVSASTPPHLSVQ 360  
Qy 361 PTGLTFYPAVDVQAFVLPNSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELK 420  
Db 361 PTGLTFYPAVDVQAFVLPNSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELK 420  
Qy 421 HSNIGPPFVELLDIMNYIVIPILVLPVNEKLOKGFPLTPARVOLYNNVLOPHQNFLLF 480  
Db 421 HSNIGPPFVELLDIMNYIVIPILVLPVNEKLOKGFPLTPARVOLYNNVLOPHQNFLLF 480  
Qy 481 GADVYK 487

RESULT 12

Db 481 GADVYK 487

RESULT 11  
US-09-861-400-15  
; Sequence 15, Application US/09861400  
; Patent No. US20020146761A1  
; GENERAL INFORMATION:  
; APPLICANT: Scott, Randal W  
; APPLICANT: Marra, Marian N  
; TITLE OF INVENTION: RECOMBINANT ENDOTOXIN-NEUTRALIZING PROTEINS  
; FILE REFERENCE: 1103/11307US01  
; CURRENT APPLICATION NUMBER: US/09/861,400  
; CURRENT FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: 08/431,517  
; PRIOR FILING DATE: 1995-05-01  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 487  
; TYPE: PRT  
; ORGANISM: human  
; FEATURE:  
; OTHER INFORMATION: human BPI amino acid (Figure 5)  
; NAME/KEY: SIGNAL  
; LOCATION: (1)..(31)  
; NAME/KEY: CHAIN  
; LOCATION: (32)..(487)  
US-09-861-400-15

Query Match 100.0%; Score 2507; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 1.7e-209;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWVSLMVLVAICTAVTAANPGVVVRI SQKGLDYASQQTAAQKEL 60  
Db 1 MRENARGPCNAPRWVSLMVLVAICTAVTAANPGVVVRI SQKGLDYASQQTAAQKEL 60  
Qy 61 KRIKIPYSDSFKIKHLKGHSFYSDMIREFQLPSSQISMVPPNVGLKFSISNANIKISG 120  
Db 61 KRIKIPYSDSFKIKHLKGHSFYSDMIREFQLPSSQISMVPPNVGLKFSISNANIKISG 120  
Qy 121 KWKAKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTTTCSSCSSHINSVHVHISKS 180  
Db 121 KWKAKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTTTCSSCSSHINSVHVHISKS 180  
Qy 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSKLOPYFQTLPMVTKIDS VAGINYL 240  
Db 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSKLOPYFQTLPMVTKIDS VAGINYL 240  
Qy 241 VAPPATTATLTDVQMKGEFYSENHNPPPPFAPVPMVEFPAADHDMVYLGSLSDYFFNTAGLV 300  
Db 241 VAPPATTATLTDVQMKGEFYSENHNPPPPFAPVPMVEFPAADHDMVYLGSLSDYFFNTAGLV 300  
Qy 301 YQAGVLKQTLRDDMI PKESKRLTTKFFGTFLPEVAKFPNMKIQIHVSASTPPHLSVQ 360  
Db 301 YQAGVLKQTLRDDMI PKESKRLTTKFFGTFLPEVAKFPNMKIQIHVSASTPPHLSVQ 360  
Qy 361 PTGLTFYPAVDVQAFVLPNSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELK 420  
Db 361 PTGLTFYPAVDVQAFVLPNSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELK 420  
Qy 421 HSNIGPPFVELLDIMNYIVIPILVLPVNEKLOKGFPLTPARVOLYNNVLOPHQNFLLF 480  
Db 421 HSNIGPPFVELLDIMNYIVIPILVLPVNEKLOKGFPLTPARVOLYNNVLOPHQNFLLF 480  
Qy 481 GADVYK 487  
Db 481 GADVYK 487

```

US-09-746-311-2
; Sequence 2, Application US/09746311
; Publication No. US20030017143A1
; GENERAL INFORMATION:
; APPLICANT: Little, II, Roger G.
; TITLE OF INVENTION: IDENTIFICATION OF NOVEL ANTIMICROBIAL AGENTS USING
; TITLE OF INVENTION: METABOLIC OXIDATION-REDUCTION INDICATOR DYES
; FILE REFERENCE: 27129/36226
; CURRENT APPLICATION NUMBER: US/09/746,311
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/143,290
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-311-2

Query Match      100.0%; Score 2507; DB 10; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.7e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPVGVVVRIISQKGLDYASQOQTAALQKEL 60
Db      1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPVGVVVRIISQKGLDYASQOQTAALQKEL 60

Qy      61 KRIPIDYDSFKIKHLGKGHSFYSDMIREFOLPSSQISMVNPVGLKFSISNANIKISG 120
Db      61 KRIPIDYDSFKIKHLGKGHSFYSDMIREFOLPSSQISMVNPVGLKFSISNANIKISG 120

Qy      121 KWKAQKRFKLMKSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180
Db      121 KWKAQKRFKLMKSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180

Qy      121 KWKAQKRFKLMKSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180
Db      121 KWKAQKRFKLMKSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180

Qy      181 KVGWLIQLFHKKIESALRNKWNQSVCEKVTNSVSSKLQPYFQTLPVMTKIDS VAGINYL 240
Db      181 KVGWLIQLFHKKIESALRNKWNQSVCEKVTNSVSSKLQPYFQTLPVMTKIDS VAGINYL 240

Qy      241 VAPPATTAETLDVQMKGEFYSNNHNPFPFAPPMVEFPAADHDMVYLGLSDYFFNTAGLV 300
Db      241 VAPPATTAETLDVQMKGEFYSNNHNPFPFAPPMVEFPAADHDMVYLGLSDYFFNTAGLV 300

Qy      301 YQEAGVLKMTLRDDMIPEKSKFRLTTKFGTFLPEVAKKFPNNMKIQIHVSASTPPHLSVQ 360
Db      301 YQEAGVLKMTLRDDMIPEKSKFRLTTKFGTFLPEVAKKFPNNMKIQIHVSASTPPHLSVQ 360

Qy      361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420
Db      361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420

Qy      421 HSNIGPFPVELLDIMNYIVPILVLRVNEKLOKGFPLPTPARVQLYNNVVLQPHQNFLLF 480
Db      421 HSNIGPFPVELLDIMNYIVPILVLRVNEKLOKGFPLPTPARVQLYNNVVLQPHQNFLLF 480

Qy      481 GADVYK 487
Db      481 GADVYK 487

RESULT 13
US-09-746-311-2
; Sequence 3, Application US/09975638B
; Publication No. US20030166528A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Jong Jye
; TITLE OF INVENTION: Antifungal Compound
; FILE REFERENCE: 27129/37753
; CURRENT APPLICATION NUMBER: US/09/975,638B
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/239,709
; PRIOR FILING DATE: 2000-10-11

```

```

; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-638B-3

Query Match      100.0%; Score 2507; DB 10; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.7e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPVGVVVRIISQKGLDYASQOQTAALQKEL 60
Db      1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPVGVVVRIISQKGLDYASQOQTAALQKEL 60

Qy      61 KRIPIDYDSFKIKHLGKGHSFYSDMIREFOLPSSQISMVNPVGLKFSISNANIKISG 120
Db      61 KRIPIDYDSFKIKHLGKGHSFYSDMIREFOLPSSQISMVNPVGLKFSISNANIKISG 120

Qy      121 KWKAQKRFKLMKSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180
Db      121 KWKAQKRFKLMKSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180

Qy      181 KVGWLIQLFHKKIESALRNKWNQSVCEKVTNSVSSKLQPYFQTLPVMTKIDS VAGINYL 240
Db      181 KVGWLIQLFHKKIESALRNKWNQSVCEKVTNSVSSKLQPYFQTLPVMTKIDS VAGINYL 240

Qy      241 VAPPATTAETLDVQMKGEFYSNNHNPFPFAPPMVEFPAADHDMVYLGLSDYFFNTAGLV 300
Db      241 VAPPATTAETLDVQMKGEFYSNNHNPFPFAPPMVEFPAADHDMVYLGLSDYFFNTAGLV 300

Qy      301 YQEAGVLKMTLRDDMIPEKSKFRLTTKFGTFLPEVAKKFPNNMKIQIHVSASTPPHLSVQ 360
Db      301 YQEAGVLKMTLRDDMIPEKSKFRLTTKFGTFLPEVAKKFPNNMKIQIHVSASTPPHLSVQ 360

Qy      361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420
Db      361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420

Qy      421 HSNIGPFPVELLDIMNYIVPILVLRVNEKLOKGFPLPTPARVQLYNNVVLQPHQNFLLF 480
Db      421 HSNIGPFPVELLDIMNYIVPILVLRVNEKLOKGFPLPTPARVQLYNNVVLQPHQNFLLF 480

Qy      481 GADVYK 487
Db      481 GADVYK 487

RESULT 14
US-09-416-828-2
; Sequence 2, Application US/09416828
; Publication No. US20030171265A1
; GENERAL INFORMATION:
; APPLICANT: Ammons, William Steve et al.
; TITLE OF INVENTION: Method of Treating Conditions Associated with
; TITLE OF INVENTION: Intestinal Ischemia/Reperfusion
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/416,828
; FILING DATE:

```

```
;
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/756,164
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/32043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-416-828-2

Query Match 100.0%; Score 2507; DB 10; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.7e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWVSLMWLVVAIGTAVTAANPGVVVRIISQKGLDYASQOQTAAALQKEL 60
Db 1 MRENARGPCNAPRWVSLMWLVVAIGTAVTAANPGVVVRIISQKGLDYASQOQTAAALQKEL 60

Qy 61 KRIKIPDYSDFKIKHLKGHSFYSDIRFQLPSSQISMVNVGLKFSISNANIKISG 120
Db 61 KRIKIPDYSDFKIKHLKGHSFYSDIRFQLPSSQISMVNVGLKFSISNANIKISG 120

Qy 121 KWKAKQRFKMGSGNFDLSIEGMSISADLKGNSPTSGKPTITCSSCSHINSVHVHISKS 180
Db 121 KWKAKQRFKMGSGNFDLSIEGMSISADLKGNSPTSGKPTITCSSCSHINSVHVHISKS 180

Qy 181 KVGMLIQLFHKKIESALRNKNSQCEKVTNSVSSKLPQFYQTLPMVTKIDSVAGINYL 240
Db 181 KVGMLIQLFHKKIESALRNKNSQCEKVTNSVSSKLPQFYQTLPMVTKIDSVAGINYL 240

Qy 241 VAPPATTAAETLDVQMGGEFYSENHNPPFPAPPVMEFFAAHDMVYLGSDYFFNTAGLV 300
Db 241 VAPPATTAAETLDVQMGGEFYSENHNPPFPAPPVMEFFAAHDMVYLGSDYFFNTAGLV 300

Qy 301 YQEAGVLKMTLRDDMI PKESKFRLLTKFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
Db 301 YQEAGVLKMTLRDDMI PKESKFRLLTKFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360

Qy 361 PTGLTFYPADVQAPAVLPNSLSASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420
Db 361 PTGLTFYPADVQAPAVLPNSLSASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420

Qy 421 HSNIGPPFVELLDIMNYIVPILVPRVNEKLOKGFPLPTPARVOLYNVLPQHFQNFLLF 480
Db 421 HSNIGPPFVELLDIMNYIVPILVPRVNEKLOKGFPLPTPARVOLYNVLPQHFQNFLLF 480

Qy 481 GADVYK 487
Db 481 GADVYK 487

RESULT 15
US-09-480-234-2
; Sequence 2, Application US/09480234
; Publication No. US20030194377A1
; GENERAL INFORMATION:
; APPLICANT: Carron, Stephen F.
; Scannon, Patrick J.
; Gavit, Patrick D.
; TITLE OF INVENTION: IMPROVED THERAPEUTIC USES OF BPI PROTEIN
; PRODUCTS IN CYSTIC FIBROSIS PATIENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
```

```
;
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/480,234
; FILING DATE: 10-Jan-2000
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/962,217
; FILING DATE: <unknown>
; APPLICATION NUMBER: 08/742,986
; FILING DATE: 1-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/34309
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-09-480-234-2
```

```
Query Match 100.0%; Score 2507; DB 10; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.7e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWVSLMWLVVAIGTAVTAANPGVVVRIISQKGLDYASQOQTAAALQKEL 60
Db 1 MRENARGPCNAPRWVSLMWLVVAIGTAVTAANPGVVVRIISQKGLDYASQOQTAAALQKEL 60

Qy 61 KRIKIPDYSDFKIKHLKGHSFYSDIRFQLPSSQISMVNVGLKFSISNANIKISG 120
Db 61 KRIKIPDYSDFKIKHLKGHSFYSDIRFQLPSSQISMVNVGLKFSISNANIKISG 120

Qy 121 KWKAKQRFKMGSGNFDLSIEGMSISADLKGNSPTSGKPTITCSSCSHINSVHVHISKS 180
Db 121 KWKAKQRFKMGSGNFDLSIEGMSISADLKGNSPTSGKPTITCSSCSHINSVHVHISKS 180

Qy 181 KVGMLIQLFHKKIESALRNKNSQCEKVTNSVSSKLPQFYQTLPMVTKIDSVAGINYL 240
Db 181 KVGMLIQLFHKKIESALRNKNSQCEKVTNSVSSKLPQFYQTLPMVTKIDSVAGINYL 240

Qy 241 VAPPATTAAETLDVQMGGEFYSENHNPPFPAPPVMEFFAAHDMVYLGSDYFFNTAGLV 300
Db 241 VAPPATTAAETLDVQMGGEFYSENHNPPFPAPPVMEFFAAHDMVYLGSDYFFNTAGLV 300

Qy 301 YQEAGVLKMTLRDDMI PKESKFRLLTKFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
Db 301 YQEAGVLKMTLRDDMI PKESKFRLLTKFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360

Qy 361 PTGLTFYPADVQAPAVLPNSLSASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420
Db 361 PTGLTFYPADVQAPAVLPNSLSASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420

Qy 421 HSNIGPPFVELLDIMNYIVPILVPRVNEKLOKGFPLPTPARVOLYNVLPQHFQNFLLF 480
Db 421 HSNIGPPFVELLDIMNYIVPILVPRVNEKLOKGFPLPTPARVOLYNVLPQHFQNFLLF 480
```

Qy 481 GADVVYK 487  
| | | | |  
Db 481 GADVVYK 487

Search completed: October 21, 2005, 11:37:01  
Job time : 174.285 secs



STIC-Biotech/ChemLib

169216

me

From: Chan, Christina  
Sent: Thursday, October 20, 2005 5:15 PM  
To: Mitra, Rita; STIC-Biotech/ChemLib  
Subject: RE: SEQ search request 10/629516

Please rush. Thanks Chris

Chris Chan  
TC 1600 New Hire Training Coordinator and SPE 1644  
(571)-272-0841  
Remsen, 3E89

RECEIVED  
OCT 21 2005  
STIC/BIOTECH/CHM LIB

-----Original Message-----

From: Mitra, Rita  
Sent: Thursday, October 20, 2005 4:16 PM  
To: Chan, Christina  
Subject: SEQ search request 10/629516

I need your approval for this search request.

I would like to request an expedited sequence search for this case because it is due this bi-week. Please search commercial and published patent databases.

10/629516

SEQ ID NO: 2,  
SEQ ID NO: 2, amino acids 10-193

Please print out the result.

Thanks.  
Rita

Rita Mitra, Ph.D.  
Patent Examiner, Art Unit 1653  
U.S. Patent and Trademark Office  
Remsen Bldg, Rm 3B65  
Alexandria, VA 22313  
(571)272-0954  
E-mail: rita.mitra@uspto.gov

3070

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

***This Page Blank (uspto)***